

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 19:46:51 ; Search time 4.05825 seconds  
(without alignments)  
7660.750 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19

Sequence: 1 taatgtcatcgccccggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
  - 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
  - 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
  - 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	86.3	2132	3	US-09-552-322-1
2	15.4	81.1	601	4	US-09-949-016-136302
3	15.4	81.1	2338	4	US-09-582-337-1
4	15.4	81.1	2350	3	US-09-187-478-1
5	15.4	81.1	2350	3	US-09-292-036-1
6	15.4	81.1	51049	4	US-09-949-016-15571
7	15	78.9	636	4	US-09-902-540-8517
8	15	78.9	6855	4	US-09-902-540-897
9	14.8	77.9	99	2	US-08-427-097-12
10	14.8	77.9	99	2	US-08-878-957-12
11	14.8	77.9	170	1	US-08-419-078-5
12	14.8	77.9	170	1	US-08-419-078-6
13	14.8	77.9	170	1	US-08-726-883-5
14	14.8	77.9	300	1	US-08-726-883-6
15	14.8	77.9	300	1	US-08-419-078-4
16	14.8	77.9	300	1	US-08-726-883-4
17	14.8	77.9	384	4	US-09-389-681-451
18	14.8	77.9	384	4	US-09-620-405B-451
19	14.8	77.9	384	4	US-09-433-828B-451
20	14.8	77.9	384	4	US-09-604-287A-451
21	14.8	77.9	384	4	US-09-834-759-451
22	14.8	77.9	384	4	US-09-590-751A-451
23	14.8	77.9	384	4	US-09-551-621-451
24	14.8	77.9	879	4	US-09-248-796A-7856
25	14.8	77.9	1322	1	US-08-419-078-1
26	14.8	77.9	1322	1	US-08-726-883-1
27	14.8	77.9	1323	4	US-09-023-655-55

c	28	14.8	77.9	1594	4	US-09-270-767-14907	Sequence 14907, A
	29	14.8	77.9	1752	1	US-08-427-097-13	Sequence 13, Appl
	30	14.8	77.9	1752	1	US-08-427-097-19	Sequence 19, Appl
	31	14.8	77.9	1752	2	US-08-878-957-13	Sequence 13, Appl
	32	14.8	77.9	1752	2	US-08-878-957-19	Sequence 19, Appl
	33	14.8	77.9	2936	4	US-09-976-594-1044	Sequence 1044, Ap
	34	14.8	77.9	28843	4	US-09-949-016-17325	Sequence 17325, A
	35	14.8	77.9	134987	4	US-09-949-016-15348	Sequence 15348, A
	36	14.8	77.9	134987	4	US-09-949-016-15349	Sequence 15349, A
	37	14.8	77.9	134987	4	US-09-949-016-15350	Sequence 15350, A
	38	14.8	77.9	134987	4	US-09-949-016-15507	Sequence 15507, A
	39	14.8	77.9	134987	4	US-09-949-016-15508	Sequence 15508, A
	40	14.8	77.9	134987	4	US-09-949-016-15509	Sequence 15509, A
	41	14.8	77.9	203475	4	US-09-949-016-14516	Sequence 14516, A
	42	14.8	77.9	203475	4	US-09-949-016-14517	Sequence 14517, A
	43	14.8	77.9	203475	4	US-09-949-016-14518	Sequence 14518, A
	44	14.8	77.9	203475	4	US-09-949-016-14519	Sequence 14519, A
	45	14.8	77.9	203475	4	US-09-949-016-17226	Sequence 17226, A

ALIGNMENTS

RESULT 1

US-09-552-322-1  
; Sequence 1, Application US/09552322  
; Patent No. 6436642  
; GENERAL INFORMATION:  
; APPLICANT: Gould-Rothberg  
; APPLICANT: Rastelli  
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING  
; FILE REFERENCE: 15966-548  
; CURRENT APPLICATION NUMBER: US/09/552,322  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR APPLICATION NUMBER: 60/130,123  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/193,203  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-552-322-1

Query Match 86.3%; Score 16.4; DB 3; Length 2132;  
Best Local Similarity 94.4%; Pred. No. 78;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19  
DB 844 AATGTCATCGTCCCCGGG 861

RESULT 2

US-09-949-016-136302  
; Sequence 136302, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 136302  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-136302

Query Match 81.1%; Score 15.4; DB 4; Length 601;  
Best Local Similarity 94.1%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 61 ATGTCATTGTCCTCCCGG 77

## RESULT 3

US-09-582-337-1/c  
; Sequence 1, Application US/09582337  
; Patent No. 6562618  
; GENERAL INFORMATION:

; APPLICANT: Japan Tobacco, Inc.  
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
; FILE REFERENCE: J1-009PCT  
; CURRENT APPLICATION NUMBER: US/09/582,337  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: JP P1997-367699  
; PRIOR FILING DATE: 1997-12-25  
; PRIOR APPLICATION NUMBER: JP P1998-356183  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 2338

TYPE: DNA

ORGANISM: Rat

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (1)..(212)

NAME/KEY: CDS

LOCATION: (213)..(1256)

NAME/KEY: 3'UTR

LOCATION: (1257)..(2338)

NAME/KEY: polyA signal

LOCATION: (2297)..(2302)

US-09-582-337-1

Query Match 81.1%; Score 15.4; DB 4; Length 2338;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 1210 ATGTCATTGTCCTCCCGG 1194

## RESULT 4

US-09-187-478-1/c  
; Sequence 1, Application US/09187478  
; Patent No. 6348329  
; GENERAL INFORMATION:

; APPLICANT: Schmidt, Brian F.  
; APPLICANT: Allen, Margaret L.  
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use  
; FILE REFERENCE: 08766/004001  
; CURRENT APPLICATION NUMBER: US/09/187,478  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2350

; TYPE: DNA  
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (212)..(1252)  
US-09-187-478-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 1209 ATGTCATTGTCCTCCCGG 1193

## RESULT 5

US-09-292-036-1/c

; Sequence 1, Application US/09292036  
; Patent No. 6358741  
; GENERAL INFORMATION:

; APPLICANT: FIBROGEN, INC  
; APPLICANT: SCHMIDT, Brian  
; APPLICANT: ALLEN, Margaret  
; APPLICANT: SVERDRUP, Fran  
; APPLICANT: CARMICHAEL, David  
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE  
; FILE REFERENCE: FIBRO100-1  
; CURRENT APPLICATION NUMBER: US/09/292,036  
; CURRENT FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: US 09/292,036  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: US 09/187,478  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0

SEQ ID NO 1

LENGTH: 2350

TYPE: DNA

ORGANISM: Rat

FEATURE:

NAME/KEY: CDS

LOCATION: (212)..(1252)

US-09-292-036-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;  
Best Local Similarity 94.1%; Pred. No. 2.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATGTCATCGTCCCGGG 19  
||||| |||||  
Db 1209 ATGTCATTGTCCTCCCGG 1193

## RESULT 6

US-09-949-016-15571/c  
; Sequence 15571, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15571  
; LENGTH: 51049  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15571

Query Match 81.1%; Score 15.4; DB 4; Length 51049;  
Best Local Similarity 94.1%; Pred. No. 3.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATGTCATCGTCCCGGG 19  
Db 13225 ATGTCATGTCCTCCCGGG 13209

## RESULT 7

US-09-902-540-8517/c  
; Sequence 8517, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 8517  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-8517

Query Match 78.9%; Score 15; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCATCGTCCCGGG 19  
Db 279 GTCATCGTCCCGGG 265

## RESULT 8

US-09-902-540-897/c  
; Sequence 897, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 897  
; LENGTH: 6855  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-897

Query Match 78.9%; Score 15; DB 4; Length 6855;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCATCGTCCCGGG 19

Db 4057 GTCATCGTCCCGGG 4043

## RESULT 9

US-08-427-097-12  
; Sequence 12, Application US/08427097  
; Patent No. 5668294  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/427,097  
; FILING DATE: 21-APR-1995  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 40-94  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 99 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "Oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-427-097-12

Query Match 77.9%; Score 14.8; DB 1; Length 99;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGG 18  
Db 79 TATTGTCATGACCCCGG 96

## RESULT 10

US-08-878-957-12  
; Sequence 12, Application US/08878957  
; Patent No. 5965796  
; GENERAL INFORMATION:  
; APPLICANT: Meagher, Richard B.  
; APPLICANT: Sommers, Anne O.  
; APPLICANT: Rugh, Clayton L.  
; TITLE OF INVENTION: Metal Resistance Sequences and  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder

```
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,957
FILING DATE: 19-JUN-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,097
FILING DATE: 21-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-878-957-12

Query Match 77.9%; Score 14.8; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TAATGTCATCGTCCCGG 18
DB 79 TATGTCATGACCCCGG 96

RESULT 11
US-08-419-078-5/c
; Sequence 5, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-419-078-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
DB 134 AATGTCATCTCCACGG 117

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-855-0572
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: Corneal Stroma
CLONE: 046611
US-08-419-078-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
DB 134 AATGTCATCTCCACGG 117

RESULT 12
US-08-419-078-6/c
; Sequence 6, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; LIBRARY: Fibroblast
; CLONE: 054216
US-08-419-078-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19
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Db 134 AATGTCATCTCCACGGG 117  
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RESULT 13  
US-08-726-883-5/c  
; Sequence 5, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Corneal Stroma  
; CLONE: 046611  
US-08-726-883-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCTCCACGGG 19  
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Db 134 AATGTCATCTCCACGGG 117  
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RESULT 14  
US-08-726-883-6/c  
; Sequence 6, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO

; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Fibroblast  
; CLONE: 054216  
US-08-726-883-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCTCCACGGG 19  
|||||

Db 134 AATGTCATCTCCACGGG 117  
|||||

RESULT 15  
US-08-419-078-4/c  
; Sequence 4, Application US/08419078  
; Patent No. 5587306  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,078  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Hybrid T/B Lymphoblast
; CLONE: 043866
US-08-419-078-4

Query Match      77.9%; Score 14.8; DB 1; Length 300;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AATGTCATCGTCCCGGG 19
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Db      256 AATGTCATCTCCACGGG 239
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Search completed: April 12, 2005, 06:04:10  
Job time : 6.05825 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 04:59:42 ; Search time 14.1055 Seconds  
(without alignments)  
8162.777 Million cell updates/sec

Title: US-09-979-558A-2

Perfect score: 19  
Sequence: 1 taatgtcatcgtccccggg 19

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	86.3	1329	17	US-10-169-395-18
2	16.4	86.3	1882	9	US-09-925-298-301
3	16.4	86.3	1882	14	US-10-102-806-301
4	16.4	86.3	1926	9	US-09-764-853-238
5	16.4	86.3	1987	9	US-09-818-143-20
6	16.4	86.3	1989	10	US-09-946-374-76
7	16.4	86.3	1989	14	US-10-006-856A-76
8	16.4	86.3	1989	14	US-10-006-818A-76
9	16.4	86.3	1989	14	US-10-006-485A-76
10	16.4	86.3	1989	14	US-10-013-907A-76
11	16.4	86.3	1989	14	US-10-015-499A-76

12	16.4	86.3	1989	14	US-10-015-393A-76	Sequence 76, Appl
13	16.4	86.3	1989	14	US-10-015-869A-76	Sequence 76, Appl
14	16.4	86.3	1989	14	US-10-012-121A-76	Sequence 76, Appl
15	16.4	86.3	1989	14	US-10-006-116A-76	Sequence 76, Appl
16	16.4	86.3	1989	14	US-10-006-117A-76	Sequence 76, Appl
17	16.4	86.3	1989	14	US-10-017-527A-76	Sequence 76, Appl
18	16.4	86.3	1989	14	US-10-013-913A-76	Sequence 76, Appl
19	16.4	86.3	1989	14	US-10-007-194A-76	Sequence 76, Appl
20	16.4	86.3	1989	14	US-10-013-430A-76	Sequence 76, Appl
21	16.4	86.3	1989	14	US-10-011-671A-76	Sequence 76, Appl
22	16.4	86.3	1989	14	US-10-012-755A-76	Sequence 76, Appl
23	16.4	86.3	1989	14	US-10-015-386A-76	Sequence 76, Appl
24	16.4	86.3	1989	15	US-10-011-692A-76	Sequence 76, Appl
25	16.4	86.3	1989	15	US-10-006-768A-76	Sequence 76, Appl
26	16.4	86.3	1989	15	US-10-017-610A-76	Sequence 76, Appl
27	16.4	86.3	1989	15	US-10-006-063A-76	Sequence 76, Appl
28	16.4	86.3	1989	15	US-10-020-063A-76	Sequence 76, Appl
29	16.4	86.3	1989	15	US-10-015-391A-76	Sequence 76, Appl
30	16.4	86.3	1989	15	US-10-017-407A-76	Sequence 76, Appl
31	16.4	86.3	1989	15	US-10-011-833A-76	Sequence 76, Appl
32	16.4	86.3	1989	15	US-10-006-041A-76	Sequence 76, Appl
33	16.4	86.3	1989	15	US-10-015-822A-76	Sequence 76, Appl
34	16.4	86.3	1989	15	US-10-015-387A-76	Sequence 76, Appl
35	16.4	86.3	1989	15	US-10-006-130A-76	Sequence 76, Appl
36	16.4	86.3	1989	16	US-10-006-172A-76	Sequence 76, Appl
37	16.4	86.3	1989	16	US-10-017-253A-76	Sequence 76, Appl
38	16.4	86.3	1989	16	US-10-015-392A-76	Sequence 76, Appl
39	16.4	86.3	1989	16	US-10-017-306A-76	Sequence 76, Appl
40	16.4	86.3	1989	16	US-10-017-867A-76	Sequence 76, Appl
41	16.4	86.3	1989	16	US-10-012-064A-76	Sequence 76, Appl
42	16.4	86.3	1989	16	US-10-013-909A-76	Sequence 76, Appl
43	16.4	86.3	1989	16	US-10-015-671A-76	Sequence 76, Appl
44	16.4	86.3	1989	16	US-10-015-610A-76	Sequence 76, Appl
45	16.4	86.3	1989	16	US-10-012-137A-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1  
US-10-169-395-18  
; Sequence 18, Application US/10169395  
; Publication No. US20040034192A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMURA, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING  
; FILE REFERENCE: 01997.015100.US  
; CURRENT APPLICATION NUMBER: US/10/169,395  
; CURRENT FILING DATE: 2002-11-29  
; PRIOR APPLICATION NUMBER: JP 2000-585  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-588  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-2299  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-26862  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: JP 2000-59367  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/JP00/09359  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 150  
; SEQ ID NO 18  
; LENGTH: 1329  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-169-395-18

Query Match 86.3%; Score 16.4; DB 17; Length 1329;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 AATGTCATCGTCCCGG 19
Db      982 AATGTCATCGTCCCGAG 999

RESULT 2
US-09-925-298-301
; Sequence 301, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1849)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-102-806-301

Query Match      86.3%; Score 16.4; DB 14; Length 1882;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AATGTCATCGTCCCGG 19
Db      529 AATGTCATCGTCCCGAG 546

RESULT 3
US-09-925-298-301
; Sequence 301, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (223)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1840)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1849)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-298-301

Query Match      86.3%; Score 16.4; DB 9; Length 1882;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AATGTCATCGTCCCGG 19
Db      529 AATGTCATCGTCCCGAG 546

RESULT 4
US-09-764-853-238
; Sequence 238, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PZ06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-853-238

Query Match      86.3%; Score 16.4; DB 9; Length 1926;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AATGTCATCGTCCCGG 19
Db      573 AATGTCATCGTCCCGAG 590

RESULT 5
US-09-818-143-20
; Sequence 20, Application US/09818143
; Patent No. US20020019000A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
; FILE REFERENCE: PB-0004 CIP
; CURRENT APPLICATION NUMBER: US/09/818,143
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 3948614CB1
; US-09-818-143-20
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Query Match 86.3%; Score 16.4; DB 9; Length 1987;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19  
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Db 716 AATGTCATCGTCCCGAG 733

## RESULT 6

US-09-946-374-76  
; Sequence 76, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
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; PRIOR FILING DATE: 1998-09-02  
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; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-15  
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; PRIOR FILING DATE: 1998-09-16  
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; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100662  
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; PRIOR APPLICATION NUMBER: 60/100664  
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; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29



US-10-006-818A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGGG 19

DB 715 AATGTCATCGTCCCGAG 732

## RESULT 9

US-10-006-485A-76

; Sequence 76, Application US/10006485A

; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2830PIC9

; CURRENT APPLICATION NUMBER: US/10/006,485A

; CURRENT FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-01

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; PRIOR FILING DATE: 1998-09-09

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;; PRIOR APPLICATION NUMBER: 60/105882  
;; PRIOR FILING DATE: 1998-10-27  
;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 AATGTCATCGTCCCGG 19

Db 715 AATGTCATCGTCCCGG 732  
RESULT 10  
US-10-013-907A-76  
; Sequence 76, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-907A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCGG 19  
Db 715 AATGTCATCGTCCCGG 732

RESULT 11  
US-10-015-499A-76  
; Sequence 76, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989



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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19
    |||||
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 12
US-10-015-393A-76
; Sequence 76, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19
    |||||
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 13
US-10-015-869A-76
; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19
    |||||
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 14
US-10-012-121A-76
; Sequence 76, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-121A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AATGTCATCGTCCCCGGG 19
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Db 715 AATGTCATCGTCCCCGAG 732

RESULT 15
US-10-006-116A-76
; Sequence 76, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
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us-09-979-558a-2.rnpb

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C15
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; CURRENT FILING DATE: 2001-12-16
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;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103678
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103679
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/103711
;	PRIOR FILING DATE:	1998-10-08
;	PRIOR APPLICATION NUMBER:	60/104257
;	PRIOR FILING DATE:	1998-10-14
;	PRIOR APPLICATION NUMBER:	60/104987
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105000
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105002
;	PRIOR FILING DATE:	1998-10-20
;	PRIOR APPLICATION NUMBER:	60/105104
;	PRIOR FILING DATE:	1998-10-21
;	PRIOR APPLICATION NUMBER:	60/105169
;	PRIOR FILING DATE:	1998-10-22
;	PRIOR APPLICATION NUMBER:	60/105266
;	PRIOR FILING DATE:	1998-10-22
;	PRIOR APPLICATION NUMBER:	60/105693
;	PRIOR FILING DATE:	1998-10-26
;	PRIOR APPLICATION NUMBER:	60/105694
;	PRIOR FILING DATE:	1998-10-26
;	PRIOR APPLICATION NUMBER:	60/105807
;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/105881
;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/105882
;	PRIOR FILING DATE:	1998-10-27
;	PRIOR APPLICATION NUMBER:	60/106023
;	PRIOR FILING DATE:	1998-10-28

Query Match	86.3%	Score 16.4;	DB 14;	Length 1989;
Best Local Similarity	94.4%	Pred. No. 1.4e+02;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19  
Db 715 AATGTCATCGTCCCCGGG 732

Search completed: April 12, 2005, 09:03:40  
Job time : 17.1055 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 19:46:51 ; Search time 325.942 Seconds  
(without alignments)  
7660.750 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
Sequence: 1 ttgatcatggctccagatt.....acctgcgggtgatacctc 1526

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	1211	79.4	269223	US-09-596-002-41	Sequence 41, Appl
2	1195	78.3	1485	US-08-299-810A-27	Sequence 27, Appl
3	1098.6	72.0	1501	US-09-793-920A-1	Sequence 1, Appl
4	1098.6	72.0	1501	US-09-821-016-5	Sequence 5, Appl
5	1098.6	72.0	1501	US-09-745-476-1	Sequence 1, Appl
6	1098.6	72.0	1501	US-09-748-205-1	Sequence 1, Appl
7	1098.6	72.0	1501	US-09-951-720-1	Sequence 1, Appl
8	1098.6	72.0	1501	US-10-411-319-1	Sequence 1, Appl
9	1098.6	72.0	1501	US-10-105-305-1	Sequence 1, Appl
10	1098.6	72.0	1501	US-10-266-787-5	Sequence 5, Appl
11	1076	70.5	1467	US-08-114-695A-1	Sequence 1, Appl
12	1070.8	70.2	1467	US-09-726-774-3	Sequence 3, Appl
13	1069.2	70.1	1542	US-08-757-653-158	Sequence 158, App
14	1069.2	70.1	1542	US-09-465-355-2	Sequence 2, Appl
15	1069.2	70.1	1542	US-08-520-946-158	Sequence 158, App
16	1069.2	70.1	1542	US-09-655-378A-158	Sequence 158, App
17	1069.2	70.1	1542	US-09-548-998E-33	Sequence 33, Appl
18	1062.6	69.6	1541	US-09-726-774-2	Sequence 2, Appl
19	1058.2	69.3	1549	US-09-492-709A-89	Sequence 89, Appl
20	1058.2	69.3	1549	US-09-492-709A-242	Sequence 242, App
21	1058.2	69.3	1549	US-09-492-709A-402	Sequence 402, App
22	1053.6	69.0	1518	US-08-114-695A-6	Sequence 6, Appl
23	1052.4	69.0	1487	US-09-726-774-14	Sequence 14, Appl
24	1039.2	68.1	1506	US-10-278-942-1	Sequence 1, Appl
25	1031.2	67.6	1500	US-09-726-774-4	Sequence 4, Appl
26	1025.2	67.2	1544	US-09-726-774-5	Sequence 5, Appl
27	1019.8	66.8	1540	US-09-228-184-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-596-002-41/c  
; Sequence 41, Application US/09596002  
; Patent No. 6632636  
; GENERAL INFORMATION:  
; APPLICANT: Legace, Robert, E.  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Berg, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: PM-0008-4 US  
; CURRENT APPLICATION NUMBER: US/09/596,002  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/140,121  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte template ID No. 6632636 41  
; PUBLICATION INFORMATION:  
US-09-596-002-41

Query Match	79.4%	Score 1211;	DB 4;	Length 269223;
Best Local Similarity	90.6%	Pred. No. 0;		
Matches 1361;	Conservative	0;	Mismatches 127;	Indels 15; Gaps 6;
Qy	30	GGCGGAGGCTTAACACATGCAATGCGAGCGGAACGATGATAGTCTGCTATTAGCGGTC	89	
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Qy	90	GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTACCTAGTAGTGGGGGATAGTCCGG 149		
Db	92900	TTAGTGGCGGACGGGTGAGTAATCTTAGGAATCTGCTAGTAGTGGGGGATAGTCCGG 92841		
Qy	150	GAATCTGCAATTAATACCGCATAGCTCTACCGGAGAAAGACGGGNTCAATTAGACCTTGC 209		
Db	92840	GAATCTGCAATTAATACCGCATAGCTCTACCGGAGAAAGACGGGNTCAATTAGACCTTGC 92785		
Qy	210	GCTATTAGATGAGCTTAAGTCGGAATTAGCTAGATGTTGGGTAAAGGCTACCATGGCGA 269		
Db	92784	GCTATTAGATGAGCTTAAGTCGGAATTAGCTAGTGGTGGGTAAAGGCTACCAAGGCGA 92725		
Qy	270	CGATCTGAGTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCGAC 329		
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QY 330 T-CTACGGAGGACGAGTGGGAAAT-----ATTGGAACAATGNGGGGAACCTGTATCCAG 383  
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QY 92664 TCCTACGGAGGACGAGTGGGGAATATGGAATTCGAACAATGGGCGAAGGCTGTATCCAG 92605  
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QY 384 CCATCCCGCGTGTGTGAAGAGGCGCTTTTGGTTGTAAAGCACTTTAAAGCAGTGAAGAAGA 443  
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QY 92604 CCATCCCGCGTGTGTGAAGAGGCGCTTTTGGTTGTAAAGCACTTTAAAGTGGGAGGAAA 92545  
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QY 444 CTCCTTCGGTTAATACCCGGGACGATGACATTAAGCTGCAGAAATAGCACCGGCTAACTCT 503  
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QY 92544 GCTTATGTTTAAATACCCCAATAGCCCTGACGTTACCCACAGAATAAGCACCGGCTAACTCT 92485  
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QY 504 GTGCCAGACGCGCGGTAAATACAGAGGTCGAAGCGTTAAATCGGAATTAATCTGGCGTAAA 563  
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QY 564 GCGAGCGTAGGTGGCTTGAATAGTCAGATGTGAATCCCGGGCTTAACTGGGAACTGC 623  
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QY 92364 ATCTGAACTGTAGGCTAGAGTAGGTGAGAGGAGTAGAATTTAGAGTGTAGCGGTGA 92305  
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QY 684 AATGCTAGAGATCTGAAGGAATACCGATGCGAAGGAGCTTCTGGCATCATCTGAC 743  
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QY 92304 AATGCTAGAGATCTGAAGGAATACCGATGCGAAGGAGCTTCTGGCATCATCTGAC 92245  
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QY 744 ACTGAGGCTCGAAAGCGTGGTAGCAACACAGGATTAGATACCTGGTAGTCCAGCCGTA 803  
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QY 92244 ACTGAGGTCGAAAGCGTGGTAGCAACACAGGATTAGATACCTGGTAGTCCAGCCGTA 92185  
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QY 804 AACGATGCTACTAGTCTGTGGTCCCTTTAGGACTTAGTACGAGCAATACGCAATAAG 863  
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QY 92184 AACGATGCTACTAGTCTGTGGTCCCTTTAAGACTTTAGTACGAGCAATACGCAATAAG 92125  
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QY 1044 ATGGCTGTCTGCTCAGTCTGTCGTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCC 1103  
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QY 1164 GAGGAAGCGGGACGAGTCAAGTCAATGCGCCCTTACGACGAGGCTACACAGTGC 1223  
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QY 91824 GAGGAAGCGGGACGAGTCAAGTCAATGCGCCCTTACGACGAGGCTACACAGTGC 91765  
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QY 1224 TACAATGGTGTACAGAGGCGAGTACACAGCGATGTGATCGGAATCTCAAAAGGCTA 1283  
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QY 91764 TACAATGGTGTACAAAGGGTTGCTACACAGCGATGTGATCGTAATCTCAAAAGGCTA 91705  
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QY 1284 TCGTAGTCCAGATTGGAGTCTGCAACTCGAATCATGAAGTAGGAATCGCTAGTAATCGC 1343  
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QY 1344 GGATCAGAAATCCCGCGGTGAATAGCTTCCCGGGCTTTGTACACACCGCGCTACACCAT 1403  
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QY 91644 AGATCAGAAATGCTCGGTGAATAGCTTCCCGGGCTTTGTACACACCGCGCTACACCAT 91585  
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QY 1404 GGGAGTTGATTGCAACAGAGTGGTTAGCTTAATCTAGTGAAGGCGGATCACCAGGTGTG 1463

Db 91584 GGGAGTTGATCTACCAGAAAGTGGTTAGCCTAACGCA-AGAGGGCGATCACACGGTGGG 91526  
QY 1464 GTCCATGACTGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTTCGGCTCGATCAC 1523  
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QY 91525 GTCCATGACTGGGTGAAGTCGTAAACAAGGTAGCCGTAGGGGAACCTTCGGCTCGATCAC 91466  
Db |||||  
QY 1524 CTC 1526  
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QY 91465 CTC 91463  
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RESULT 2  
US-08-299-810A-27  
; Sequence 27, Application US/08299810A  
; Patent No. 5721097  
; GENERAL INFORMATION:  
; APPLICANT: Roseau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE  
; TITLE OF INVENTION: DETECTION OF BRANHAMELLA CATARRHALIS STRAINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5721097west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,810A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.70-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1485 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; IMMEDIATE SOURCE:  
; CLONE: 16S rRNA Gene  
; US-08-299-810A-27  
Query Match 78.3%; Score 1195; DB 1; Length 1485;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1352; Conservative 0; Mismatches 128; Indels 12; Gaps 7;  
QY 36 AGCTTAACACATGCAAGTCGAGCGGAACGATAGTCTTATAGCGCTCGAGCNG 95  
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QY 1 AGCTTAACACATGCAAGTCGAAAG--AAGTTAGGAAGCTTGC--TTCTGATCTTAGTG 56  
Db |||||  
QY 96 CCGGAGCGGTGAGTAATCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGGGGAACT 155  
Db |||||  
QY 57 GCGGAGCGGTGAGTAATCTTAGGAATCTAGTCTAGTAGTGGGGATAGCTTGGGAACT 116  
Db |||||  
QY 156 CGAATTAATACCGCATAGTCTACGGGAGAAACAGCGGNTATTAGACCTTCGGCTATT 215  
Db |||||  
QY 117 CAAGCTAATACCGCATACGACCTACGCGTGAAGGGGG-----CTTTTAGCTCTCGCTATT 172  
Db |||||

QY	216	AGATGAGCCTAAAGTCCGGATTAGCTAGATGGTGGGTAAAGGCTTACCAATGGCGACGATCT	275
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QY	276	GTAGCTGTGCTGAGAGGATGATCAGCCACACCGGACTTGAGACACGGCCCGGACT-CTAC	334
DB	233	GTAGCTGTGCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCGAGACTCTCTAC	292
QY	335	GGGAGGCAGAGTGGGGAATATGGACAATGGNGGAAACCTGTATCCAGCCATGTCGCGT	394
DB	293	GGGAGGCAGAGTGGGGAATATGGACAATGGGCGAAAGCCTGATCCAGCCATGTCGCGT	352
QY	395	GTGTGAAGAGCCCTTTTGGTTGTAAAGCACTTTTAAAGCAGTGAAGAAGCACTTTCGGTTA	454
DB	353	GTGTGAAGAGCCCTTTTGGTTGTAAAGCACTTTTAAAGTGGGAGGAGAAAGCTTATGGTTA	412
QY	455	ATACCCGGGGACGATGACATTTAGCTGCGAATTAAGCACCGGCTTAACCTGTGCCAGCAGC	514
DB	413	ATACCCATAAGCCCTGACGTTACCCACAGAATAGCACCGGCTTAACCTGTGCCAGCAGC	472
QY	515	CGCGTAAATACAGAGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGTAGG	574
DB	473	CGCGTAAATACAGAGGTGCAAGCGTTAATCGG-ATTACTGGGCGTAAAGCGCGCTAGG	531
QY	575	TGGCTTGAATAGTCAGATGTGNAATCCCGGGCTTAACTGGGAACTGCATCTGNAACTG	634
DB	532	TGGTTATTTTAAAGTCAGATGTGAAAGCCCGGGCTTAACTGGGAACTGCATCTGATAC	591
QY	635	TTAGGCTAGAGTGGGTGAGAGGGAAGTAGAATTTTCAGGTGTAGCGGTGAAATGCGTAGAG	694
DB	592	GATAACTAGATAGGTGAGAGGGNGTAGAATTCAGGTGTAGCGGTGAAATGCGTAGAG	651
QY	695	ATCTGAAGGAATACCGATGGCGAAGGAGCTTCTTCGGCATCATACTGACACTGAGGCTCG	754
DB	652	ATCTGGAGGAATACCGATGGCGAAGGAGCTCCCTGGCATCATACTGACACTGAGGTCG	711
QY	755	AAAGCTGGGTAGCAACAGAGTTAGTACCCTGGTGTGTCACGCCGTAAACGATGTCTA	814
DB	712	AAAGCTGGGTAGCAACAGAGTTAGTACCCTGGTGTGTCACGCCGTAAACGATGTCTA	771
QY	815	CTAGTCTGTGGGTCCCTTGGAGACTTTAGTGACGCACTTAAACGCAATAGTAGACCGCCTG	874
DB	772	CCAGTCTGTGGTCTTTTAAAGACTTAGTGACGCACTTAAACGCAATAGTAGACCGCCTG	831
QY	875	GGGAGTACGGCCGCAAGTTTAAACTCAAATGAAATTGACGGGGGCCGCAACAGCGGTGG	934
DB	832	GGGAGTACGGCCGCAAGTTTAAACTCAAATGAAATTGACGGGGGCCGCAACAGCGGTGG	891
QY	935	AGCATGTGGTTTAAATTCGATCGAACGCAAGAACCTTACTGTGTCTTGACATACACAGAA	994
DB	892	AGCATGTGGTTTAAATTCGATCGAACGCAAGAACCTTACTGTGTCTTGACATAGTGAGAA	951
QY	995	TCTTGTAGAGATACGAGAGTGCCCTTCGGGAATTTGTATACAGGTGCTGCATGGGTGTCGT	1054
DB	952	TCTTGCAGAGATGCGAGAGTGCCCTTCGGGAATTCACATACAGGTGCTGCATGGGTGTCGT	1011
QY	1055	CAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCCCTTAGT	1114
DB	1012	CAGCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGTCCCTTAGT	1071
QY	1115	TACCAGCACTTCGGGTGGGAACCTTAAGGATACTGCCAGTCACAAAACCTGGAGGAGGCGG	1174
DB	1072	TACCAGCGACTTCGGTGGGGAACCTTAAGGATACTGCCAGTGCACAACTGGAGGAGGCGG	1131
QY	1175	GGACGAGCTCAAGTCATCATGGCCCTTACGACCGAGGCTACACAGCTGCTACAATGGTAG	1234
DB	1132	GGACGAGCTCAAGTCATCATGGCCCTTACGACCGAGGCTACACAGCTGCTACAATGGTAG	1191
QY	1235	GTAACAGGGCGAGCTACACAGGATGTGATCGGAATCTCAAAAAGCCTATCGTAGTCAG	1294
DB	1192	GTAACAAAGGGTGTGTACACAGCGATGTGATGCTAATCTCAAAAAGCCTATCGTAGTCAG	1251

### RESULT 3

US-09-793-920A-1

US-09-153-920A-1  
; Sequence 1. Application US/09793920A

Sequence 1, Application No. 6479621

; FACEIL NO. 6475621  
; GENERAL INFORMATION:

GENERAL INFORMATION:  
APPLICANT: Canon Inc.

\* APPLICANT: CANON INC.  
\* TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as  
\* monomer unit, and method for producing the same.  
\* TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as

FILE REFERENCE: 4396021

FILE REFERENCE: 4396021  
CURRENT APPLICATION NUMBER: US/09/793.920A

; CURRENT APPLICATION NUMBER: US/0  
 ; CURRENT FILING DATE: 2001-02-28

; CURRENT FILING DATE: 2  
 : NUMBER OF SEO ID NOS: 1

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; NUMBER OF SEQ
; SEQ ID NO 1

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; SEQ ID NO 1
:
: LENGTH: 1501

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LENGTH: 1501  
TYPE: DNA

; TYPE: DNA  
; ORGANISM: *Pseudomonas jessenii* 161 strain

; ORGANISM: PS  
IIS-08-793-930A-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;

Query Match 72.0%; Score 1038.0  
Best Local Similarity 85.9%; Pred. No. 0;

Best Local Similarity 85.5%; Fied. NO: 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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QY  
30 GGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATGATAGCTTGCTATAGGCGTC 89

Db 9 GCGGCAGGCCCTAACACATGCAGTCCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

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Db 67 G--CGGCGACGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGACAAAGTCTC 123

QY 150 GAAACTCGAATTAAATACCGCATACGT-CTACGGGAGAAAGCAGGGNTCATTAGACCTTG 208

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QY 209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGTAAGGCCCTACCATGGCG 268

Db 184 CGCTATCAGATGAGCCTAGGTCCGATTAGCTAGTTGGTGAGGTAATGGCTCA CCAAGGG 243

DB 184 CGCTATCAGATGAGCCTAGGTCGGAATTAGCTAGTTGGTGAAGTAAATGGCTCACCAAGCG 243

QY 269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCCGA 328

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Qy 329 CT-CTACGGGAGGCAGCAGTGGGAAATA TTGGACAATGGNGGGAACCTTGATCCAGCCAT 387

Db 304 CTCCACGGAGGCAGCAGTGGGGAATATTGGACAATGGCGAAAGCCTGATCCAGCCAT 363

Db 484 CAGCAGCCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGC 543  
Qy 568 GCGTAGGTGGCTTGATAAGTCAGATGTGAATATCCCGGGCTTAACTCTGGGAATGCAATCT 627  
Db 544 GCGTAGGTGGCTTGATAAGTTGGATGTGAAGCCCGGGCTCAACTGGGAATGCAATTC 603  
Qy 628 GAAACTGTTAGCTAGCTAGGTAGAGGGAGTAGAATTTTCAGGTGTAGCGGTGAATG 687  
Db 604 AAAACTGACAGCTAGATGTGGTAGAGGGTGGTGAATTTTCCTGTGTAGCGGTGAATG 663  
Qy 688 CGTAGAGATCTCAAGGAATACCGATGGCGAAGGAGCTTCTCGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGACACAGCTGGCGAAGGCGACCACTGGAATGATGACTGACACTG 723  
Qy 748 AGGCTCGAAGCGTGGGTAGCAACACAGATTTAGATACCTCGGTAGTCACCGCGTAAACG 807  
Db 724 AGGTGCGAAGCGTGGGAGCAACACAGATTTAGATACCTCGGTAGTCACCGCGTAAACG 783  
Qy 808 ATGTCTACTAGTCTGGTCCCTTGAGGACTTGTAGCGAGCTTGTAGCGAGCTTAAGTGA 867  
Db 784 ATGTCAACTAGCTGGAGCCCTTGGAGCTTGTAGTGGCGAGCTTAAGTGA 843  
Qy 868 CCGCTCGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTTGACGGGGCCCGCACAA 927  
Db 844 CCGCTCGGGAGTACGGCGCAAGGTTAAACTCAAAATGAATTTGACGGGGCCCGCACAA 903  
Qy 928 GCGGTGAGCATGTGTTTAAATTCATGACCAACGCGAAGAACCTTACCTGGTTCCTGACNTA 987  
Db 904 GCGGTGAGCATGTGTTTAAATTCATGACCAACGCGAAGAACCTTACCGAGGCTTGAATC 963  
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Db 964 CAATGAATTTCCAGAGATGATGGTGGCTTTCGGGAATTTGTATACAGGTGCTGCAATG 1023  
Qy 1048 CTGTCGTAGCTCGTGTGAGATGTGGGTAACTCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTCGTAGCTCGTGTGAGATGTGGGTAACTCCGCAACGAGCGCAACCTTGT 1083  
Qy 1108 CCTTAGTTACAGCAC-TTCGGGTGGNACTTAAAGTACTAGGACTGACAGTGAACAATCGAG 1166  
Db 1084 CCTTAGTTACAGCACGTAATGGTGGGACCTTAAGGAGACTGCGGGTGACAAACCGGAG 1143  
Qy 1167 GAAGCGGGGACGACGTCAAGTCAATCGGCCCTTACGACCGAGGCTACACAGCTGCTAC 1226  
Db 1144 GAAGTGGGATGACGTCAAGTCAATCGGCCCTTACGGCTGGGCTACACAGTGTAC 1203  
Qy 1227 AATGGTAGTACAGAGGACGTACACAGCATGTGATGCAATCTCAAAAAGCCTATCG 1286  
Db 1204 AATGGTCGGTACAGAGGTTTCCCAAGCGCGAGGTGGAGCTTAATCCCAACAAACCGATCG 1263  
Qy 1287 TAGTCCAGATGGAGTCTGCAACTCGACTCCATCAAGTAGGAATCGGTAGTAATCGCGGA 1346  
Db 1264 TAGTCCGATCGCAGTCTGCAACTCGACTCGGTGAAGTGGGAATCGGTAGTAATCGCGGA 1323  
Qy 1347 TCAGAAATGCCCGGTGAATAGCTTCCCGGGCTTGTACACACCGCCCGTACACACCATGGG 1406  
Db 1324 TCAGAAATGCCCGGTGAATAGCTTCCCGGGCTTGTACACACCGCCCGTACACACCATGGG 1383  
Qy 1407 AGTTGATGACCAAGAGTGTGAGCTAA-CTTAGTAGAGGGCGATCACACGGTGTGGT 1465  
Db 1384 AGTGGGTGACCAAGAGTGTGAGCTAACTTCCGGAGGACGCTTACACCGGTGTGAT 1443  
Qy 1466 CGATGACTGGGGTGAAGTCGTAAACAGTAGCCGTAGCGGAACCTCGGGCTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCGTAAACAGTAGCCGTAGGGNAACCTCGGGCTGGATCAC 1501

## RESULT 4

US-09-821-016-5  
; Sequence 5, Application US/09821016  
; Patent No. 6485951  
; GENERAL INFORMATION:  
; APPLICANT: CANON INC.

; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 4051021  
; CURRENT APPLICATION NUMBER: US/09/821.016  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO. 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161; BP-7376  
; FEATURE:  
US-09-821-016-5

## Query Match

Best Local Similarity 72.0%; Score 1098.6; DB 4; Length 1501;

Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGGCAGGCTTAACACATCGAATCGAGCGGAACCATGATAGCTTGTCTATTAGGCGTC 89  
Db 9 GCGGCAGGCTTAACACATCGAATCGAGCGG--ATGACGGAGCTTGTCTCTGAATTC 66  
Qy 90 GAGCNGCGGACGCGGTGAGTAATCTTATGGAATCTACTAGTGTGGGGATAGCTCGGG 149  
Db 67 G---CGCGGACGCGGTGAGTAATCTGCTAGGAATCTGCTGTAGTGGGACACGCTC 123  
Qy 150 GAAACTCGAATTAATACCGCATACGT-CTAGCGGAGAAACGAGGGGNTCAATTAGACCTG 208  
Db 124 GAAAGGACGCTAATACCGCATACGCTCTACGGGAGAAACGAGGGGACCTTCGGGGCTT 183  
Qy 209 CGCTATTAGATGAGCCCTAAGTTCGAGTGTAGTGTGGGTAAAGCCCTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCCCTAGTTCGAGTGTAGTGTGGTGAATTAAGCTTACCAGGCG 243  
Qy 269 ACATCTGTAGTGTCTGAGAGATGATCAGCCACACCGGACTGAGACACGCGCCCGGA 328  
Db 244 ACATCTGTAACTGGTCTGAGAGATGATCAGTCACTGGAACCTGAGACACGCGTCAGA 303  
Qy 329 CT-CTAGCGGACGACGAGTGGGGAATTTGGCAATTTGGNGGAACCTCTAGCCAGCAT 387  
Db 304 CTCTACGGGAGGACGAGTGGGGAATTTGGCAATTTGGGCGAAAGCCCTGATCAGGCAT 363  
Qy 388 GCGCGGTGTGGAAGAGGCTTTTGGTGTAAAGCACCTTTAAGCAGTGAAGAAGACTCT 447  
Db 364 GCGCGGTGTGGAAGAGGCTTTTGGGATTTGAAGCACCTTTAAGTGGGAGGAAGGCAT 423  
Qy 448 TCGGTTAATACCGGGGACGATGACATTAAGTGTGAGAAATTAAGCACCGGCTAACTCTGTC 507  
Db 424 TAACTTAATACGTTAGTGTGTTTGGACGTTACCGACAGAAATTAAGCACCGGCTAACTCTGTC 483  
Qy 508 CAGCAGCGCGGTAATACAGAGGCTGCAAGCGTTAATCGGAATTTACTGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAATACAGAGGCTGCAAGCGTTAATCGGAATTTACTGGCGTAAAGCGG 543  
Qy 568 GCGTAGTGGCTTTGATAAGTTCAGATGTGAATCCCGGGCTTAACTTGGGAACCTGCACT 627  
Db 544 GCGTAGTGGCTTTGTTAAGTTGATGTGAAGCCCGGGCTCAACCTGGGAACTGCAATTC 603  
Qy 628 GAACTGTTAGCTAGATGAGTGAAGGAGTGAATTTTCAAGTGTAGCGGTGAATG 687  
Db 604 AAAACTGACAAAGCTAGATGAGTGAAGGAGTGAATTTTCTGTGTAGCGGTGAATG 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTCGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGACACACAGTGGCGAAGGCGACCACTGGAATGATGACTGACACTG 723  
Qy 748 AGGCTCGAAGCGTGGGTAGCAACACAGGATTAATACCTGTGTAGTCCACCGCGTAAACG 807  
Db 724 AGGTGCGAAGCGTGGGAGCAACACAGGATTAATACCTGTGTAGTCCACCGCGTAAACG 783  
Qy 808 ATCTCTACTAGTGTGGGTCCCTTGGAGCTTTAGTGAAGCACTTACGAGCAGCAACGCAATTAAGTGA 867  
Db 784 ATGTCAACTAGCCGTTGGGAGCCCTTGGAGCTTGTAGTGGCGACGCTTAACGCTTAAGTTGA 843





QY 1227 AATGGTAGGTACAGAGGCGACCTACACAGCGATGTGATCGAATCTCAAAAGCCTATCG 1286  
Db |||||  
QY 1204 AATGGTCGGTACAGAGGGTTCCAAAGCGCGAGGTGAGCTTAATCCCAAAAACCGATCG 1263  
Db |||||  
QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCATCAAGATGAGAAATCGGTAGTAATCGCGGA 1346  
Db |||||  
QY 1264 TAGTCCGAGTCGAGTCTGCAACTCGACTGCGTGAAGTTCGGAATCGCTAGTAATCGCGAA 1323  
Db |||||  
QY 1347 TCAGAAATGCCCGGTGAATACGTTCCCGGGCTTTGTACACACCGCCCGTCAACCATGGG 1406  
Db |||||  
QY 1324 TCAGAAATGTCGGGTGAATACGTTCCCGGGCTTTGTACACACCGCCCGTCAACCATGGG 1383  
Db |||||  
QY 1407 AGTTGATTGCACACAGAGTGTGAGCTAA-CTTAGTGAGGGCGATCACACGCTGTGGT 1465  
Db |||||  
QY 1384 AGTGGGTGACACAGAGTGTGAGCTAACTTTCCGGAGGACGCTTACACCGGTGTGAT 1443  
Db |||||  
QY 1466 CGATGACTGGGGTCAAGTCTGTAACAGGTAGCCGTAGGGAACTCGGGCTTGAATCAC 1523  
Db |||||  
QY 1444 TCATGACTGGGGTGAAGTCTGTAACAGGTAGCCGTAGGGNAACCTGGGCTGGATCAC 1501  
Db |||||

RESULT 6  
US-09-748-205-1  
; Sequence 1, Application US/09748205  
; Patent No. 6586562  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism  
; TITLE OF INVENTION: those are used for the method.  
; FILE REFERENCE: 4351009  
; CURRENT APPLICATION NUMBER: US/09/748,205  
; CURRENT FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain.  
US-09-748-205-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGCGAGGCTTACACATGCAAGTCTGAGCGGAACGATGATAGCTTGTCTATTAGGCGTC 89  
Db |||||  
QY 9 GCGCGAGGCTTACACATGCAAGTCTGAGCGG--ATGACGGGAGCTTGTCTCTGAATTC 66  
Db |||||  
QY 90 GAGCNGCGGACGGGTGAGTAATCTTAGGAATCTACTAGTAGTGGGGATAGCTCGGG 149  
Db |||||  
QY 67 G---CGGGGACGGGTGAGTAATCTGCTAGGATCTGCTGTAGTGGGGACACGCTCTC 123  
Db |||||  
QY 150 GAAACTCGAATTAATACCGCATAGCT-CTAGCGGAGAAAGCAGGGGNTCAATTAGACCTTG 208  
Db |||||  
QY 124 GAAAGGACGCTAATACCGCATAGCTCTTACGGGAGAAAGCAGGGGACCTTGGGGCTTG 183  
Db |||||  
QY 209 CGCTATTAGTACGCTTAAGTCGATGATGATGATGATGATGATGATGATGATGATGATG 268  
Db |||||  
QY 184 CGCTATTAGTACGCTTAAGTCGATGATGATGATGATGATGATGATGATGATGATGATG 243  
Db |||||  
QY 269 ACATCTGTAGTCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 328  
Db |||||  
QY 244 ACATCTGTAGTCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 303  
Db |||||  
QY 329 CT-CTACGGGAGGACGATGGGAAATATTGGAATATTGNGGGAACCTTATGACGATGAT 387  
Db |||||  
QY 304 CTCTACGGGAGGACGATGGGAAATATTGGAATATTGNGGGAACCTTATGACGATGAT 363  
Db |||||  
QY 388 GCGCGGTGTGAGAGAGGCTTTTGTCTTAAGCACTTTAGCACTGAGAGACTCT 447  
Db |||||  
QY 364 GCGCGGTGTGAGAGAGGCTTTTGTCTTAAGCACTTTAGCACTTGAAGTGGGAGGAGG 423  
Db |||||  
QY 448 TCGGTTAATACCGGGGACGATGATGATGATGATGATGATGATGATGATGATGATGATG 507  
Db |||||

RESULT 7

US-09-951-720-1  
; Sequence 1, Application US/09951720  
; Patent No. 6635782  
; GENERAL INFORMATION:  
; APPLICANT: Canon Kabushiki Kaisha  
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof  
; FILE REFERENCE: 4477001  
; CURRENT APPLICATION NUMBER: US/09/951,720  
; CURRENT FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: JP 279900/2000  
; JP 378827/2000  
; JP 165238/2001  
; JP 165509/2001  
; JP 275063/2001  
; PRIOR FILING DATE: 2000-09-14  
; 2000-12-13  
; 2001-05-31  
; 2001-05-31  
; 2001-09-11  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161 strain.  
US-09-951-720-1

Query Match 72.0%; Score 1098.6; DB 4; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 0; Mismatches 202; Indels 9; Gaps 6;  
Matches 1287; Conservative 0;

QY 30 GCGCGAGCGTTAAACATGCAAGTCGAGCGGAAACGATGATGATCTTCTATTAGCGCTC 89  
DB 9 GCGCGAGCGCTTAACATGCAAGTCGAGCGG--ATGACGGAGCTTCTCTCTGAATCA 66

QY 90 GAGCGCGGAGCGGTGATGATTAATCTTAGGAACTACCTAGTAGTGGGGGATAGTCCGG 149  
DB 67 G---CGGCGGAGCGGTGATGATTAATCTTAGGAACTACCTAGTAGTGGGGGACACGCTC 123

QY 150 GAACTCGAATTAATACCGCATACCT-CTACGGGAGAAAGCGGGNTCATTAGACCTTG 208  
DB 124 GAAAGGAGCGTAAATACCGCATACCTCTACGGGAGAAAGCGGGGACCTTCGGGCGCTTG 183

QY 209 CGCTATTAGATGAGCTAAGTCGATGATGATGATGATGATGATGATGATGATGATGATG 268  
DB 184 CGCTATCAGATGAGCTAGTGGGATGATGATGATGATGATGATGATGATGATGATGATG 243

QY 269 AGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328  
DB 244 AGCATCCGTAACCTGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATG 303

QY 329 CT-CTACGGGAGCGAGTGGGGAATATTGGACAATGNGGGAACCTGATCCAGCCAT 387  
DB 304 CTCCTACGGGAGCGAGTGGGGAATATTGGACAATGNGGGAACCTGATCCAGCCAT 363

QY 388 GCGCGGTGTGGAAGAGCGCTTTTGGTTGTAAGCACTTTAAGCAGTGAAGAAGACTCT 447  
DB 364 GCGCGGTGTGGAAGAGCGCTTTCGGATTGTAAGCACTTTAAGTGGAGAGGCGAT 423

QY 448 TCGGTTAATACCGGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 507  
DB 424 TAACTTAATACCGTTAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 483

QY 508 GAGCAGCGCGGTAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGAATTAATCG 567  
DB 484 GAGCAGCGCGGTAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGAATTAATCG 543

QY 568 GCGTAGGTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 627  
DB 544 GCGTAGGTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 603

QY 628 GAACTGTAGCTAGTGTAGGAGGAGTGAATTTTACAGGTGTAGCGGTGAATG 687  
DB 604 AAACTGACAGCTAGTGTAGGAGGAGTGAATTTTCTGTGTAGCGGTGAATG 663

QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTGGCATCATACTGACACTG 747  
DB 664 CGTAGATATAGGAAGGAACACCACTGGCGAAGGCGCACCACTGGACTGATCTGACACTG 723

QY 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGATTAGATACCTCTGGTGTGTCACCGCGTAACG 807  
DB 724 AGGTGCGAAAGCGTGGGAGCAAAACAGATTAGATACCTCTGGTGTGTCACCGCGTAACG 783

QY 808 ATGTCTACTAGTCTGTGGTCCCTTGGAGCTTGTAGCGAGCTTAACGCAATAGTAGA 867  
DB 784 ATGTCAACTAGCTGTGGAGCTTGTAGTGGCGAGCTTAACGCAATAGTAGA 843

QY 868 CCGCTGGGAGTACGCGCGCAAGCTTAAACTCAAAATGAATTGACGGGGGCCCGCACAA 927  
DB 844 CCGCTGGGAGTACGCGCGCAAGCTTAAACTCAAAATGAATTGACGGGGGCCCGCACAA 903

QY 928 GCGGTGAGCATGTGGTTTAAATTCGATGCAACGGAAGAACCTTACCTGCTTGTGACATA 987  
DB 904 GCGGTGAGCATGTGGTTTAAATTCGAAACGGAAGAACCTTACCGAGGCTTGTGACATC 963

QY 988 CACAGAACTTGTAGAGATACGAGAGTCCCTTCGGGAATTTGTATACAGGTGCTGCATGG 1047  
DB 964 CAATGAACCTTTCAGAGATGATGGTGCCTTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

QY 1048 CTGTCTGCTAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTGT 1107  
DB 1024 CTGTCTGCTAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTGT 1083

QY 1108 CCTTAGTTACAGCAC--TTCGGGTGGGAATCTTAAGGATATGCGAGTGAACAACTGAG 1166  
DB 1084 CCTTAGTTACAGCACCGTAATGTTGGGCACTCTAAGGAGACTGCGCGTGAACAAACCGGAG 1143

QY 1167 GAAGCGGGAGCAGCTCAGTCATCTGCGCCCTTACGACCAGGCTTACACAGTGTCTAC 1226  
DB 1144 GAAGTGGGGATGACGTCAGTCATCTATGCGCCCTTACGCGCTGGGCTACACAGTGTCTAC 1203

QY 1227 AATGCTAGGTACAGAGGCGAGCTACAGCGCATGTGATCGGAATCTCAAAAGCCCTATCG 1286  
DB 1204 AATGCTCGGTACAGAGGTTGCCAAGCGCGAGGTGGAGCTAATCCCAACAAACCGATCG 1263

QY 1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCATGAAAGTGAAGTAACTGCTAGTAACTCGCGGA 1346  
DB 1264 TAGTCCGAGTCCGACTCTGCAACTCGACTCGTGGTGAAGTCCGAACTGCTAGTAACTCGCGGA 1323

QY 1347 TCAGAAATGCGCGGTGAATACGTTCCCGGGCTTTGTACACACCGCGCTCACACCATCGG 1406  
DB 1324 TCAGAAATGCGCGGTGAATACGTTCCCGGGCTTTGTACACACCGCGCTCACACCATCGG 1383

QY 1407 AGTTGATTGCAACCAAGATGTTAGCCTAA--CTTAGTGAGGGCGATCACACGGTGTGGT 1465  
DB 1384 AGTGGTTGCAACCAAGATGTTAGCCTAATCTTCGGGAGGACGGTTACCAACGGTGTGAT 1443

QY 1466 CGATGACTGGGGTGAAGTCTGTAACAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523  
DB 1444 TCATGACTGGGGTGAAGTCTGTAACAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501

## RESULT 8

US-10-411-319-1  
; Sequence 1, Application US/10411319  
; Patent No. 6649381  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms  
; FILE REFERENCE: In The Same  
; FILE REFERENCE: 03500.015001.1  
; CURRENT APPLICATION NUMBER: US/10/411,319  
; CURRENT FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: US 09/748,205  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

Query Match      72.0%; Score 1098.6; DB 4; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGCTTAAACACATGCAAGTCGAGCGGAACGATGATAGCTTGTCTATTAGGCGTC 89
Db 9 GCGCGCAGCTTAAACACATGCAAGTCGAGCGG--ATGACGGGACCTTGTCTTCTGAAATCA 66
Qy 90 GAGCNGCGGAGCGGCTGAGTAACTCTTAGGAATCTAAGTGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGGCGGACGGGTGAGTAACTCTAGGAATCTGCTGTGTAGTGGGGGACACAGCTCTC 123
Qy 150 GAACTCGAATTATACCGCATAGT-CTACGGGAGAAACGAGGGNTCAATTAGACCTTG 208
Db 124 GAAAGGACGCTAATACCGCATAGTCTCTACGGGAGAAACGAGGGACCTTTCGGGCGCTTG 183
Qy 209 CGCTATTAGTAGAGCTTAAAGTCGATGATGCTAGATGCTGGGTAAAGGCTTACCATGGCG 268
Db 184 CGCTATCAGATGAGCTTAGTTCGATGCTAGTGTGCTAGGTAATGGCTCACCAAGCG 243
Qy 269 ACATCTGTAGCTGTCTGAGAGGATGATACGCCACACCGGGAATGAGACACGCGCCCGGA 328
Db 244 ACATTCGCTTAACCTGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGCGTCCGA 303
Qy 329 CT-CTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAACCTCTGATCAGGCAAT 387
Db 304 CTCCTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAAGCTGATCAGGCAAT 363
Qy 388 GCGCGCTGTGTGAAGAAGGCGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db 364 GCGCGCTGTGTGAAGAAGGCTCTCGGATTTGAAGCACTTTAAGTTCGGAGGAAGGCGAT 423
Qy 448 TCGGTTAATACCGGGACGATGATAGTCTGAGAAATAGCAACCGGCTAACTCTGTGC 507
Db 424 TAACCTAATAGCTTGTGTTTGTAGCTTACCGACAGAAATAGCAACCGGCTAACTCTGTGC 483
Qy 508 CAGCAGCGCGGTAATACAGAGGTCGAAGCTTAACTCGGAATTAATCTGGGCGTAAAGCGGA 567
Db 484 CAGCAGCGCGGTAATACAGAGGTCGAAGCTTAACTCGGAATTAATCTGGGCGTAAAGCGG 543
Qy 568 GCGTAGTGGCTTGAATAGTCAGATGTAATCCCGGGCTTAACTGGGAATCTGCAATCT 627
Db 544 GCGTAGTGGCTTGTAAAGTGGATGTCAAAGCCCGGGCTCAACCTGGGAATCTGCATTC 603
Qy 628 GAACTGTAGGCTAGGTCAGAGGGAAGTAGAATTCAGGTGTAGGGTGAATG 687
Db 604 AAAAAGTGAAGCTAGAGTATGAGAGGCTGAGGAAATTCCTGTGTAGCGGTGAATG 663
Qy 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGCGAGCTTCTTGGCATCATACTGACACTG 747
Db 664 CGTAGATATAGGAAGGAACACCACTGGGGAAGGCGACCACTGGAATGATGACACTG 723
Qy 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGATTAAGTATACCTGGTGTAGTCCACCGCGTAAACG 807
Db 724 AGGTGCGAAAGCGTGGGAGCAAAACAGATTAAGTATACCTGGTGTAGTCCACCGCGTAAACG 783
Qy 808 ATGCTACTAGTCTGCTGGTCTTGGAGCTTATAGTACCGAGCTTACCGAATTAAGTGA 867
Db 784 ATGTCAACTAGCTGCTGGAGCTTGGAGCTTATAGTGGCGAGCTTACCGATTAAGTTGA 843
Qy 868 CCGCTCGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTCAGCGGGGCGCGCAAA 927
Db 844 CCGCTCGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTCAGCGGGGCGCGCAAA 903
Qy 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACGCGGAAGACCTTACCTGGTCTTGAATA 987
Db 904 GCGGTGAGCATGTGTTTAAATTCGATGCAACGCGGAAGACCTTACCGAGGCTTGAATC 963

RESULT 9
US-10-105-305-1
; Sequence 1, Application US/10105305
; Patent No. 6777153
; GENERAL INFORMATION:
; APPLICANT: CANON KABUSHIKI KAISHA
; TITLE OF INVENTION: POLYHYDROXYALKANOATE CONTAINING UNIT WITH THIENYL STRUCTURE IN THE
; TITLE OF INVENTION: CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER B
; TITLE OF INVENTION: TONER WHICH CONTAIN THIS POLYHYDROXYALKANOATE, AND IMAGE-FORMING
; TITLE OF INVENTION: IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER
; FILE REFERENCE: CPO16309
; CURRENT APPLICATION NUMBER: US/10/105,305
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551
; PRIOR FILING DATE: 2001-3-27, 2001-4-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-10-105-305-1

Query Match      72.0%; Score 1098.6; DB 4; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy 30 GCGCGCAGCTTAAACACATGCAAGTCGAGCGGAACGATGATAGCTTGTCTATTAGGCGTC 89
Db 9 GCGCGCAGCTTAAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGTCTTCTGAAATCA 66
Qy 90 GAGCNGCGGAGCGGCTGAGTAACTCTTAGGAATCTAAGTGTAGTGGGGGATAGCTCGGG 149
Db 67 G---CGGCGGACGGGTGAGTAACTCTAGGAATCTGCTGTGTAGTGGGGGACACAGCTCTC 123
Qy 150 GAACTCGAATTATACCGCATAGT-CTACGGGAGAAACGAGGGNTCAATTAGACCTTG 208
Db 124 GAAAGGACGCTAATACCGCATAGTCTCTACGGGAGAAACGAGGGACCTTTCGGGCGCTTG 183
Qy 209 CGCTATTAGTAGAGCTTAAAGTCGATGATGCTAGATGCTGGGTAAAGGCTTACCATGGCG 268
Db 184 CGCTATCAGATGAGCTTAGTTCGATGCTAGTGTGCTAGGTAATGGCTCACCAAGCG 243
Qy 269 ACATCTGTAGCTGTCTGAGAGGATGATACGCCACACCGGGAATGAGACACGCGCCCGGA 328
Db 244 ACATTCGCTTAACCTGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGCGTCCGA 303
Qy 329 CT-CTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAACCTCTGATCAGGCAAT 387
Db 304 CTCCTACGGGAGGACAGATGGGGAATATTGGCAATGNGGGAAAGCTGATCAGGCAAT 363
Qy 388 GCGCGCTGTGTGAAGAAGGCGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db 364 GCGCGCTGTGTGAAGAAGGCTCTCGGATTTGAAGCACTTTAAGTTCGGAGGAAGGCGAT 423
Qy 448 TCGGTTAATACCGGGACGATGATAGTCTGAGAAATAGCAACCGGCTAACTCTGTGC 507
Db 424 TAACCTAATAGCTTGTGTTTGTAGCTTACCGACAGAAATAGCAACCGGCTAACTCTGTGC 483
Qy 508 CAGCAGCGCGGTAATACAGAGGTCGAAGCTTAACTCGGAATTAATCTGGGCGTAAAGCGGA 567
Db 484 CAGCAGCGCGGTAATACAGAGGTCGAAGCTTAACTCGGAATTAATCTGGGCGTAAAGCGG 543
Qy 568 GCGTAGTGGCTTGAATAGTCAGATGTAATCCCGGGCTTAACTGGGAATCTGCAATCT 627
Db 544 GCGTAGTGGCTTGTAAAGTGGATGTCAAAGCCCGGGCTCAACCTGGGAATCTGCATTC 603
Qy 628 GAACTGTAGGCTAGGTCAGAGGGAAGTAGAATTCAGGTGTAGGGTGAATG 687
Db 604 AAAAAGTGAAGCTAGAGTATGAGAGGCTGAGGAAATTCCTGTGTAGCGGTGAATG 663
Qy 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGCGAGCTTCTTGGCATCATACTGACACTG 747
Db 664 CGTAGATATAGGAAGGAACACCACTGGGGAAGGCGACCACTGGAATGATGACACTG 723
Qy 748 AGGCTCGAAAGCGTGGGTAGCAAAACAGATTAAGTATACCTGGTGTAGTCCACCGCGTAAACG 807
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Db 844 CCGCTCGGAGTACGCGCGCAAGGTTAAACTCAAAATGAATTCAGCGGGGCGCGCAAA 903
Qy 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACGCGGAAGACCTTACCTGGTCTTGAATA 987
Db 904 GCGGTGAGCATGTGTTTAAATTCGATGCAACGCGGAAGACCTTACCGAGGCTTGAATC 963
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Db 338 ACUUCUACGGGAGCAGAGUGGGGAAUUAUUCGCAAAUUGGGCGCAAGCCUGAUGCAGCCA 397  
Qy 387 TGCCCGCGTGTGTGAAGAGCCCTTTTGGTTGTAAAGACTTTAAGCAGTGAAGAGACTC 446  
Db 398 UGCGCGUGUAGUAGAGAGCCUUCGUGUUAAGUUAUUCAGCGGGGAGAGGAG 457  
Qy 447 TTCGGTTAATACCCGGGAGCAGATGATTCATGCTGAGATAAGCACCAGCTTACTCTGTG 506  
Db 458 UAAAGUUAUAUCCUUGCUAUGAUGUUAUCCCGCAGAGAGCACCAGCUAACCCGUG 517  
Qy 507 CCAGCAGCGCGGTAAATACAGAGGCTGCAAGCTTAAATCGGAATTAATCGGCTAAAGCG 566  
Db 518 CCAGCAGCGCGGUAUAUCCGAGGGUGCAAGCGUUAUCCGGAUUAUCCGCGCUAAGCG 577  
Qy 567 AGCGTAGGTGGCTGATAGTCAGATGTGAATCCCGGGCTTAACCTGGGAATCGATC 626  
Db 578 CACGAGCGGUGUUAAGUCAGUAGUUAUCCCGGCUACCTCGGAGUUAUGCAUC 637  
Qy 627 TGAATCTTTAGGTAGAGTGGTGAAGGAGTGAATTTTCAAGTGTAGCGTGAAT 686  
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Qy 687 GCGTAGAGATCTGAAGGATACCGATGCGAGGAGCTTCTCGCATCATCTACACT 746  
Db 698 GCGUAGAGAUUGGAGGAAUCCGUGGCGAAGCGGCGCCUGGACGAAAGCUGACGU 757  
Qy 747 GAGGCTCGAAAGCGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCAGCCGTAAC 806  
Db 758 CAGGUGCGAAGCGUGGGGAGCAAAACAGGAUUAUCCUGUAGUCCAGCGCUUAAC 817  
Qy 807 GATGCTACTAGTCTGGTCCCTTGGAGACTTAGTGACGCGAGCTTAACCAATTAAGTAG 866  
Db 818 GAUGUGCAUUGGAGGUGUCCUUGAGGCGUGGCUUCCGAGCUAACCGGUAAGUGC 877  
Qy 867 ACCGCTGGGAGTAGCGCCGCAAGTTAAACTCAATGAATTCACGCGGGCCGCA 926  
Db 878 ACCGCTGGGAGUAGCGCGCAAGGUAUAAACUCAAAUGAAUUGACGGGGCGCGCA 937  
Qy 927 AGCGGTGAGCATGTGTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT 986  
Db 938 AGCGGUGAGCAUGUGUUAUUCGUAUGCAACGCGAAGAACCUUACUGUUGUAGCAU 997  
Qy 987 ACACAGAATCTTGTAGATACAGAGTGCCTTCGGGAATTGTGATACAGGTGTCATG 1046  
Db 998 CCACGAAGUUAUUCAGAGAGAAUGUGCCUUCGGGAACCGUGAGACAGGUGUGCAUG 1057  
Qy 1047 GCTGTCGTGCTGTCGTGAGATGTTGGTTAAGTCCGCAACGAGCGCAACCTTG 1106  
Db 1058 GCGUGGUGACGUGUGUUGAAUUGUGGUAAGUCCCGCAACGAGCGCAACCCUUA 1117  
Qy 1107 TCCTTTAGTACCAGCATTTCCGGTGGGAATCTTAAGGATCTGCCAGTGACAACTGGAG 1166  
Db 1118 UCCUUGUUGCCAGCGGUGCCGCGGAACUCUAAAGGAGACUGCCAGUUAUACUGGAG 1177  
Qy 1167 GAAGCGGGGACGCTCAAGTCAATGCGCCCTTACGACAGGCGCTACACATGCTAC 1226  
Db 1178 GAAGUGGGGAGUAGCUCAAGUUAUGCCUUAUCCAGCAGGCGUACACAGGUGUAC 1237  
Qy 1227 AATGTTAGTACAGAGGCGAGCTACACAGCATGTGATCGGAATCTCAAAAGCCTATCG 1286  
Db 1238 AAUGCGCAUAAAGAGAGCGACUCCGCGAGAGCAAGCGACCUCAUAAAGUGCGUGC 1297  
Qy 1287 TAGTCCAGATTGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346  
Db 1298 UGUCGGAUUGGAGUUGCAACUCGACUCCAUAGAUGCGGAUUCGUGUAUUCUGGA 1357  
Qy 1347 TCAGAAATCCCGGTGAATAGCTTCCCGGGCTTGTACACACCGCCCGCTACACCATGGG 1406  
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Qy 1407 AGTTGATTCACAGAGAGTGGTTAGCTTAACTTAGTGAGGCGGATACACAGGTGTGT 1465  
Db 1418 AGUGGUGUAAAAGUAGUAGUUAUCCUUGGGGAGCGGCUUACCAUUCUUGUAGU 1477

Qy 1466 CGATCACTGGGTGAAGTCTGTAACAAAGGTAGCCGTAGGGAACTTGGCGTGCATCCT 1525  
Db 1478 UCAUGACUGGGUGAAGUCGUAACAAAGUUAACCGUAGGGGAACCUUGCGUUGAUCACU 1537  
Qy 1526 C 1526  
Db 1538 C 1538

RESULT 12  
US-09-726-774-3  
; Sequence 3, Application US/09726774  
; Patent No. 6677153  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Anticibense Antibacterial Method and  
; FILE REFERENCE: Composition  
; CURRENT APPLICATION NUMBER: US/09-726,774  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1467  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-726-774-3

Query Match 70.2%; Score 1070.8; DB 4; Length 1467;  
Best Local Similarity 85.9%; Pred. No. 0;  
Matches 1233; Conservative 0; Mismatches 199; Indels 4; Gaps 4;  
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Db 29 GCGGACCGGTGAGTAACTTAGGAATCTCGCTAGTAGTGGGGAACAACGTTTCGAAAG 88  
Qy 155 TCGAATTAATACCCATACGT-CTACGGGAGAAACAGGGGNTCAATTAGACTTGGCTA 213  
Db 89 GAAACGCTAATACCCATACGTCTACGGGAGAAACAGGGGACCTTCGGGCTTCGGCTA 148  
Qy 214 TTAGATGAGCCCTAAGTTCGGATTAGCTAGATGGTGGGTAAGGCTCAATCGGACGAT 273  
Db 149 TCAGATGAGCCCTAGTTCGGATTAGCTAGTGGTGAAGTAAACGCTCAACAGGCGCAT 208  
Qy 274 CTGTAGTGTCTGAGAGGATGATCAGCAACCGGGACTGAGACACCGGCGGACT-CT 332  
Db 209 CCGTAACCTGCTGAGAGGATGATCAGTCACTGGAACCTGAGACACCGGTCAGACTCT 268  
Qy 333 ACGGGAGCAGCTGGGGAATATGGCAATGNGGAAACCTGATCCAGCCATGCCGC 392  
Db 269 ACGGGAGCAGCTGGGGAATATGGCAATGNGGAAACCTGATCCAGCCATGCCGC 328  
Qy 393 GTGTGTGAAGAGCGCTTTGTTGTAAAGCACTTTAAGCAGTGAAGAGACTCTTCGT 452  
Db 329 GTGTGTGAAGAGCGCTTCGGAATTTGAAGCACTTTAAGTGGGAGGAGGCGATTACC 388  
Qy 453 TAATACCGGGGAGCAGTACATTAAGTGAAGTAAGCAACCGGCTTAATCTGTGCGAGA 512  
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Qy 513 GCGGCTTAATACAGAGGTCAGAGCTTAATCGAATTAATCGGCTTAAGAGCGGCTA 572  
Db 449 GCGGCTTAATACAGAGGTCAGAGCTTAATCGAATTAATCGGCTTAAGAGCGGCTA 508  
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Db 509 GGTGCTTGAATGATGTAATCGGCTTAATCGGCTTAAGAGCGGCTA 568  
Qy 633 TGTTAGGCTAGAGTAGGTGAGAGGAGTGAATTTTCAAGTGTAGCGGTGAATCGGTAG 692

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Db 569 TGGCAAGCTAGATATGGCAGAGGGTGGTGGAAATTTCTCTGTGTAGCGGTGAAATGCGTAG 628
Qy 693 AGATCTGAAGGAATACCGATGGCGAAGCGAGCTTCTCTGGCATCATCTGACACTGAGGCT 752
Db 629 ATATAGGAAGGAACACCAAGTGGCGAAGCGCACCCTGGGCTAATCTGACACTGAGGTTG 688
Qy 753 CGAAAGCGTGGGTAGCAACAGGATTAGATACCTCTGTAGTCCACGCGGTAAACGATGTC 812
Db 689 CGAAAGCGTGGGAGCAACAGGATTAGATACCTCTGTAGTCCACGCGGTAAACGATGTC 748
Qy 813 TACTAGTCGTTGGTCCCTTGGAGCTTAGTGAACGAGCTAAACGCAATAAGTAGACCGCC 872
Db 749 GACTAGCGTGGGATCTTGGATCTTGGAGCTTAGTGGCGCAGCTAAACGCAATAAGTCGACCGCC 808
Qy 873 TGGGAGTAGCGCGCAAGGTTAAACCTCAATGAATTTGACGCGGGGCCCGCACAGCGGT 932
Db 809 TGGGAGTAGCGCGCGCTAGGTTAAACCTCAATGAATTTGACGCGGGGCCCGCACAGCGGT 868
Qy 933 GGAGCATGTGTTAAATTCGATGCAACGCGAAGCACTTACCTGGTCTTGACATACACAG 992
Db 869 GGAGCATGTGTTAAATTCGAGCAACGCGAAGCACTTACCTGGTCTTGACATACACAG 928
Qy 993 AATCTTTAGAGATACGAGAGTGCCTTTCGGGAATTTGTATACAGGTGCTCATGGCTGTC 1052
Db 929 AACTTTCCAGAGATGGATTTGGTCTTTCGGGAATTTGTATACAGGTGCTCATGGCTGTC 988
Qy 1053 GTAGCTCGTGTGCTGATGTTGGGTTAAGTCCGCAACGAGCGCAACCTTGTCTCTTA 1112
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Qy 1113 GTTACCAGCAC- TTCGGGTGGGAATCTTAAGGATGCTGCGAGTACCAAACTGGAGGAAG 1171
Db 1049 GTTACCAGCACGTTAAGTGGGCACTCTAAGGAGACTGCGCGGTGACAAAACGAGGAGG 1108
Qy 1172 CGGGAGCAGCTCAAGTCATCATGGCCCTTACGACAGGGCTACACAGTGTCTACAATGG 1231
Db 1109 TGGGGATGACGTCAGTCAATGCTGCTTACGCGCTTACGCGCTTACACAGTGTCTACAATGG 1168
Qy 1232 TAGGTACAGAGGCGAGCTACACAGGATGCTGCGAATCTCAAAAGCCTATGCTAGTC 1291
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Db 1229 CGGATCGAGTCTGCAACTCGACTCGTGAAGTGGGAATCGCTAGTAATCGTGAATCAGA 1288
Qy 1352 ATGCCCGCGTGAATACGTTCCCGGCTTGTATACACAGCGCGCTACACACCATGGAGTTG 1411
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Db 1349 GTTGCTCCAGAGTAGCTAGTCTAACCTTCGGGGGAGCGGTTACCAAGGAGGTTATTCATG 1408
Qy 1471 ACTGGGTGAAGTCGTAAACAGGTAGCGGTAGGGGAACCTTGGGCTGGATCACCTC 1526
Db 1409 ACTGGGTGAAGTCGTAAACAGGTAGCGGTAGGGGAACCTTGGGCTGGATCACCTC 1464
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## RESULT 13

US-08-757-653-158

; Sequence 158, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen &amp; Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

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; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-653-158
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Query Match 70.1%; Score 1069.2; DB 2; Length 1542;  
Best Local Similarity 83.7%; Pred. No. 0;  
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;

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Qy 30 GCGGCGAGGCTTAAACATGCAAGTCGAGCGGAAC- GATGATAGCTTGTATATAGCGT 88
Db 38 GCGGCGAGGCTTAAACATGCAAGTCGAGCGGAACGTAACAGGAAGCTTGTCTTTCTG 97
Qy 89 CGAGCGCGGCGGCTGAGTAACTTCTAGGAATCTACCTAGTAGTGGGGGATAGCTCGG 148
Db 98 ACAGTGGCGGAGCGGTGAGTAACTCTGCGGAACCTGCCTGATGAGGGGGGTAACACT 157
Qy 149 GGAACCTCGAATTAATACCGCAT- ACGTCTACGGGAGAAAGCAGGGGNTCATTAGACCTT 207
Db 158 GGAACCGGTAGTAAATACCGCATAAACGTCGCAAGACCAAGAGGGGACCTTCGGGCTC 217
Qy 208 GCCTATTAGATGAGCTTAAGTCGGATTAGCTAGTGGTGGGTAAAGCCTACCATGGC 267
Db 218 TTGCCATCGGATGTGCCAGATGGGATTAGCTAGTGGGTGGGTAAACGCTCACCTAGGC 277
Qy 268 GACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGAATGAGACAGGGCCCGG 327
Db 278 GAGATCCCTAGCTGGTCTGAGAGGATGACAGCCACACTGGAACTGAGACACGGTCCAG 337
Qy 328 ACT-CTACGGGAGCAGCAGTGGGGAATATTTGGAACAATGNGGGAAACCTGTATCCAGCCA 386
Db 338 ACTCTAGCGGAGCAGCAGTGGGGAATATTTGGAACAATGNGGGAAACCTGTATCCAGCCA 397
Qy 387 TCGCGGTGTGTGAAGAGGCTTTTGGTTGTAAGCACTTTAAGCACTGAAGAGACTC 446
Db 398 TCGCGGTGTGTGAAGAGGCTTTTGGTTGTAAGCACTTTAAGCACTGAAGAGAGGAG 457
Qy 447 TCGGTGTAATACCCCGGAGCAGTGAATTAAGCTGCAAGATAAGCAGCGGTAACTCTGTG 506
Db 458 TAAAGTTAATACCTTTGCTCATTTGACGTTACCCGAGAGAGACCGGCTAACTCCGTG 517
Qy 507 CCAGCAGCCCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCTGGCGGTAAAGCG 566
Db 518 CCAGCAGCCCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCTGGCGGTAAAGCG 577
Qy 567 AGCGTAGGTGCTTGAATAGTCAGATGTAAGTCCCGGGCTTAAACCTGGGAACCTGCATC 626
Db 578 CAGCAGCGGCTTTGTTTAAAGTCAGATGTGAATATCCCGGGCTCAACCTGGGAACCTGCATC 637
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Qy 638 TCATACCTGCAAGCTTGAGTCTCGTAGAGGGGGTAGAATTCAGGTGTAGCGGTGAAT 697
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Qy 687 CGGTAGAGATCTGAAGGAATACCGATGCGGAGGAGCTTCTGTCATCATCTACACT 746
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Qy 747 GAGGCTCGAAAGCGTGGGTAGCAAAACAGATTAGATACCTGTGTAGTCCAGCCGTAAC 806
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Qy 758 CAGGTGCGAAGCGTGGGAGCAAAACAGATTAGATACCTGTGTAGTCCAGCCGTAAC 817
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Qy 807 GATGTCTACTAGTCCGTTGGTCCCTTGGAGGACTTAGTACGCGAGCTAACGCAATAAGTAG 866
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Qy 867 ACCGCTGGGAGTAGCGGCGCAAGGTTAAACTCAATGAAATTGACGGGGGCGGCA 926
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Qy 878 ACCGCTGGGAGTAGCGGCGCAAGGTTAAACTCAATGAAATTGACGGGGGCGGCA 937
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Qy 938 AGCGGTGAGCATGTGTTTAACTCGATGCAACGCGAAGACCTTTACCTGTGTTGACAT 997
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Qy 987 ACACAGAATCTGTAGACATACGAGATGCGCTTCGGGAATTTGTATACAGGTGCTGATG 1046
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Qy 998 CCACGGAAGTTTCAGAGATGAGATGTGCTTCCGGAACCGTGAGACAGGTGCTGATG 1057
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Qy 1058 GCTGTGCTGAGTCTGCTGCTGAGATGTTGGTTAAGTTCGCGCAACGAGCGCAACCTTG 1117
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Qy 1118 TCCTTTAGTTACAGCACTTCGGTGGGAATCTTAAGATGACTGCGAGTGACAACTGAG 1177
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Qy 1227 AATGTTAGTACAGGCGAGCTACACAGCATGTGATGCGAATCTCAAAAGCGCTATCG 1286
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Qy 1238 AATGCGCATCAAAAGAGAGCGACCTCGCAGAGCAAGCGGACCTCATNAAGTGCCTCG 1297
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Qy 1298 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGTGA 1357
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Qy 1407 AGTTGATTGACCAAGAGTGTGTTAGCTTAACTTTAGTACAGGCGGATCACACGCTGTGGT 1465
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Qy 1418 AGTGGGTTGCAAAAGAGTAGGTAGCTTAACTTTAGTACAGGCGGCTTACCACTTTGTGAT 1477
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Qy 1466 CGATGACTGGGCTGAAGTCGTAAACAAGTACCGTAGGGGAACCTGCGGCTGGATCACT 1525
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Qy 1478 TCATGACTGGGCTGAAGTCTGTAAACAGGTAACTGAGGGGAACCTGCGGTTGGATCACT 1537
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1526 C 1526
Db 1538 C 1538
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## RESULT 14

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US-09-465-355-2
; Sequence 2, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
```

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; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 2620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1542
; TYPE: RNA
; ORGANISM: Escherichia coli
; US-09-465-355-2
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## Query Match

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Best Local Similarity 70.1%; Score 1069.2; DB 3; Length 1542;
Matches 1009; Conservative 247; Mismatches 241; Indels 4; Gaps 4;
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Qy 38 GCGCGCAGGCGUAACACAUGCAAGTCGAACGGUAACAGGAAGAACUUGUUCUUGUG 97
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 89 CGAGCNGCGGACCGGTGAGTAATCTTAGGAATCTTACTAGTAGTGGGGATAGCTCGG 148
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 98 ACAGAGUGCGGACCGGUGAGUAUGUCUGGGAACUCGCUUGAGGAGGGAUAACUACU 157
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 149 GGAACCTCGAATTAATACCGCAT-ACGTCTACGGGAGAAACAGCGGNTCAATTAGACCTT 207
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Qy 158 GGAACCGUAGCUAAUACCGCAUACGUGCAAGACCAAGAGGGGGACCUUGCGGCCUC 217
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 208 GCGCTATTAGATGAGCTTAAGTCGATAGTGTAGTGGGTAAAGGCTTACCATGCGC 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 218 UUGCCUUGGAGUGGCCAGAUUGGUAUGCUAGUGGUGGUAACGGCUCACCUAGGC 277
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 268 GACCATCTGTAGCTGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGCGCCGG 327
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Qy 278 GACGAUCCUAGCUGGUCUGAGAGAGUACCAAGCCACACUGGAACUGAGACACGGUCCAG 337
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 328 ACT-CTACGGGAGCAGCAGTGGGGAATAATTGGACAATGNGGGAACCTGATCCAGCCA 386
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Qy 338 ACUCUACGGGAGCAGCAGUGGGGAAUUAUGCAAUUGGCGCAAGCGCUGAUGCAGCCA 397
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Qy 387 TGCCGCTGTGTGAAGAGGCTTTTGGTTGTAAGCACCTTTAAGCAGTGAAGAGACTC 446
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Qy 398 UGCGCGUGUUAAGAAGAGGCCUUUCGGUGUUAAGUAUUUUCAGCGGGAGGAGGAG 457
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 447 TTCGGTTAAATACCGGGGACGATGACATTAGCTCAGAAATAAGCACCGGCTAACTCTGTG 506
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Qy 507 CCAGCAGCCCGGTAAATACAGAGGTCAGAGGTAATTCGGAATTTACTGGCGCTAAAGCG 566
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Qy 518 CCAGCAGCCCGGUUAUACCGAGGUGGUAACGCUUAUUCGGAUUAUUCUGGCGUUAAGCG 577
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 567 AGCGTAGGCTGTGTAAGTCAAGTGAATCCCGGGCTTAACTGGGAACTGCATC 626
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 578 CACGAGGCGUUUUAAGUAGUAGUAAUCCCGGGGCUCAACCTGGGAACTGCAUC 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 627 TGAACCTGTAGGCTAGATAGGTGAGAGGGAAGTAGAATTTACAGGTGTAGCGGTGAAT 686
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Qy 638 UGAUACUGGCAAGCUUGUCUUGAGAGGGGGUAGAAUUCUCCAGGUGAGCGGUGAAU 697
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Qy 687 GCGTAGAGATCTGAAGGAATACCGATGCGGAAGCAGCTTCTCTGGCATCATCTGACACT 746
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Db 698 GCGUAGAUUCUGGAGGAUACCGGUGCGAAGCGGCCCCCGGACGAGACUAGCGCU 757
Qy 747 GAGGCTCAAAAGCTGGTAGCAAAACAGGATTAGATACCTCTGGTAGTCCAGCGGTAAAC 806
Db 758 CAGGUGCAAAAGCTGGGAGCAAAACAGAUUAGAUACCCUGUAGUACCGCGGUAAC 817
Qy 807 GATGCTACTAGTCTGGTCCCTTGGAGGACTTAGTGACCGACGATCAACCAATAGTAG 866
Db 818 GAUGUGCAUUGGAGUGUGCCUUGAGGCGUGCUUCCGGAGCUAACCGGUUAAGUCG 877
Qy 867 ACCGCTGGGAGTACCGCCGCAAGGTTAAATCAAAATGAATTCAGCGGGGCCCGCAC 926
Db 878 ACCGCTGGGAGUACGCGCGCAAGGUUAAACUCAAUAGAUUAGACGGGGCCCGCAC 937
Qy 927 AGCGTGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACTCTGCTTTGACAT 986
Db 938 AGCGUGGAGCAUGUGGUUUAUUGAUGCAACGCAAGCAACCUUACUGGUCUUGACAU 997
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Db 1358 UCAGAAUCCACGUGAAUACUUCUCCGGGCUUUGUACACACACCGCCGUCACACCAUGG 1417
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Qy 1466 CGATGACTGGGTCGTAAGTCGTAACAGGTAGCCGTAGGGAAACCTGCGGCTGGATCACCT 1525
Db 1478 UCAUGACUGGGUAGUAGUUAACAGUAAACCGUAGGGGAAACCGUGGUGUAGUACCU 1537
Qy 1526 C 1526
Db 1538 C 1538
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## RESULT 15

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US-08-520-946-158
; Sequence 158, Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
```

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; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-158
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Query Match 70.1%; Score 1069.2; DB 3; Length 1542;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1256; Conservative 0; Mismatches 241; Indels 4; Gaps 4;

Qy 30 GCGCGCAGCGCTTAACACATGTCGACGCGAAAC-GATGATAGCTTGTATAGCGGT 88
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Qy 507 CAGACGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTCTGGGCGTAAAGCG 566
Db 518 CCAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAAGTCTGGGCGTAAAGCG 577
Qy 567 AGCGTAGGTGGCTTGTAAAGTGCAGATGTGAAATCCCCGGGCTTAACTCTGGGAATCATC 626
Db 578 CAGCAGCGCGGTTTGTAAAGTGCAGATGTGAAATCCCCGGGCTTAACTCTGGGAATCATC 637
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 04:59:42 ; Search time 1132.89 Seconds  
(without alignments)  
8162.777 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
Sequence: 1 ttgtatcgctccagat.....acctgctggtgatcacctc 1526

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues  
Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB1.seq:\*

19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1211	79.4	269223	17	US-10-672-787-41
2	1098.6	72.0	1501	9	US-09-745-476-1
3	1098.6	72.0	1501	9	US-09-821-016-5
4	1098.6	72.0	1501	9	US-09-748-205-1
5	1098.6	72.0	1501	9	US-09-793-920A-1
6	1098.6	72.0	1501	9	US-09-951-720-1
7	1098.6	72.0	1501	10	US-09-791-610-1
8	1098.6	72.0	1501	14	US-10-218-519-5
9	1098.6	72.0	1501	14	US-10-266-787-5
10	1098.6	72.0	1501	14	US-10-252-518-5
11	1098.6	72.0	1501	14	US-10-105-305-1

12	1098.6	72.0	1501	15	US-10-133-404A-1
13	1098.6	72.0	1501	16	US-10-242-696-1
14	1098.6	72.0	1501	17	US-10-411-319-1
15	1098.6	72.0	1501	17	US-10-649-646-1
16	1098.6	72.0	1501	17	US-10-603-996-1
17	1098.6	72.0	1501	18	US-10-827-670-1
18	1098.6	72.0	1501	18	US-10-007-725-5
19	1098.6	72.0	1501	18	US-10-007-725-5
20	1098.6	72.0	1501	18	US-10-007-725-5
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23	1098.6	72.0	1501	18	US-10-007-725-5
24	1098.6	72.0	1501	18	US-10-007-725-5
25	1098.6	72.0	1501	18	US-10-007-725-5
26	1098.6	72.0	1501	18	US-10-007-725-5
27	1098.6	72.0	1501	18	US-10-007-725-5
28	1098.6	72.0	1501	18	US-10-007-725-5
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30	1098.6	72.0	1501	18	US-10-007-725-5
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43	1098.6	72.0	1501	18	US-10-007-725-5
44	1098.6	72.0	1501	18	US-10-007-725-5
45	1098.6	72.0	1501	18	US-10-007-725-5

ALIGNMENTS

RESULT 1  
US-10-672-787-41/c  
; Sequence 41, Application US/10672787  
; Publication No. US20040067554A1  
; GENERAL INFORMATION:  
; APPLICANT: LAGACE, Robert, E.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BERG, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: ELITRA.025C1  
; CURRENT APPLICATION NUMBER: US/10/672.787  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 09/596,002  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
US-10-672-787-41

Query Match 79.4%; Score 1211; DB 17; Length 269223;  
Best Local Similarity 90.6%; Pred. No. 0;  
Matches 1361; Conservative 0; Mismatches 127; Indels 15; Gaps 6;  
Qy 30 GCGCGAGGCTTAACACATGCAAGTCGAGCGAAGCATGATAGCTTCTATTAGCGCTC 89  
Db 92956 GCGCGAGGCTTAACACATGCAAGTCGAGCGAAGCATGATAGCTTCTATTAGCGCTC 92901  
Qy 90 GAGCNGCCGAGCGGTAGTAACTTAGGAACTTACCTAGTAGTGGGGGATAGCTCGG 149  
Db 92900 TTAGTGGCGGAGCGGTAGTAACTTAGGAACTTACCTAGTAGTGGGGGATAGCTCGG 92841

QY	150	GAAACTCGAATTAAATACCCGATACGCTTACCGGAGAAAGCAGGGGNTCAATTAAGACTTGC	209
Db	92840		92785
		GAAAACCAAGCTAATATACCGATACGACTACGGGTGAAGGGGG---CTTTAGCTCTC	
QY	210	GCTATTAGATGAGCCTAAAGTCGATTAGCTAGATGTTGGGTAAAGGCTTACCATGGCGA	269
Db	92784		92725
		GCTATTAGATGAGCCTAAAGTCGATTAGCTTGGTTGGTGGGTAAAGGCCCTACCAAGGGCA	
QY	270	CGATCTGTAGTGGTCTTGAGAGGATGATCAGCCACAACCGGAGCTGAGACACGCGCCCGGAC	329
Db	92724		92665
		CGATCTGTAGTGGTCTTGAGAGGATGATCAGCCACACTCGGACTGAGACACGCGCCCGAC	
QY	330	T-CTACCGGAGGACGAGTGGGGAAT-----ATTGCAATATGNGGGGAACCTGATCCAG	383
Db	92664		92605
		TCCTACCGGAGGACGAGTGGGGAATATTGGATTGGACAAATGGGCGGAAGCCTGATCCAG	
QY	384	CCATGCCCGCTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGA	443
Db	92604		92545
		CCATGCCCGCTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAAGTGGGGAGGAAGA	
QY	444	CTCTTCGGTTAAATACCCGGGAGCGATGACATTAGCTGCAGATAAAGCAACCGGCTAACTCT	503
Db	92544		92485
		GCTTATGTGTTAATACCCATAAAGCCCTGAGCTTACCACAGAAATAAGCACCGGCTAACTCT	
QY	504	GTGCCAGCACCGCGGTAAATACAGAGGGTGAAGCGTTAATCGGAATTACTTGGGCGTAAA	563
Db	92484		92425
		GTGCCAGCACCGCGGTAAATACAGAGGGTGAAGCGTTAATCGGAATTACTTGGGCGTAAA	
QY	564	CGCAGCCTAGTGGCTTGATTAAGTCAAGATGTGAATCCCGGGCTTAACTGGGAACCTGC	623
Db	92424		92365
		CGCGCGCTAGTGGTTATTATTAAGTCAAGATGTGAAGCCCGGGCTTAACTGGGAACCTGC	
QY	624	ATCTGAACCTGTTAGCTAGATGAGTGAGAGGAGTAGAATTTCCAGGTGACGGTGA	683
Db	92364		92305
		ATCTGATCTGGAATACTAGATGAGTGAGAGGAGTAGAATTTCCAGGTGACGGTGA	
QY	684	AATGCGTPAGATCTCTGAAGGAATACCGATTGGCAAGGCAGCTTCTTGGCATCATCTGAC	743
Db	92304		92245
		AATGCGTPAGATCTCTGAAGGAATACCGATTGGCAAGGCAGCTTCTTGGCATCATCTGAC	
QY	744	ACTGAGCTCGAAGCGTGGGTAGCAAAACAGATTAGATACCTCGGTAGTCCAACCGGTA	803
Db	92244		92185
		ACTGAGTGGCAAGCGTGGGTAGCAAAACAGATTAGATACCTCGGTAGTCCAACCGGTA	
QY	804	AACGATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTACGCAGACTTAACGCAATAAG	863
Db	92184		92125
		AACGATGTCTACTAGTCGTTGGGTCTTTTAAAGACTTAGTGACGCAGTTAACGCAATAAG	
QY	864	TAGACCGCTGGGGAGTACGCGCGAAGGTTAAAACTCMAATGAATTGACGGGGGCGCGC	923
Db	92124		92065
		TAGACCGCTGGGGAGTACGCGCGAAGGTTAAAACTCMAATGAATTGACGGGGGCGCGC	
QY	924	ACAAGCGTGGAGCATGTGGTTTAAATTCGATCAACGCGGAACCTTACCTGTGTTGA	983
Db	92064		92005
		ACAAGCGTGGAGCATGTGGTTTAAATTCGATCAACGCGGAACCTTACCTGTGTTGA	
QY	984	CATACAAGAACTCTTGAGAGTACGAGAGTCCCTTCGGGAATTGTGATCAGGTGCTGC	1043
Db	92004		91945
		CATAGTGAGAACTCTTGAGAGTACGAGAGTGCCTTCGGGAATTCACATACAGGTGCTGC	
QY	1044	ATGGCTGTGTCAGCTCGTTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCC	1103
Db	91944		91885
		ATGGCTGTGTCAGCTCGTTCGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCC	
QY	1104	TTGTCTCTTAGTTACCAAGCACTTCGGGTGGGAACCTCTAAGGATACTGCCAGTGACAAACTG	1163
Db	91884		91825
		TTTTCCTTAGTTACCAAGCACTTCGGGTGGGAACCTCTAAGGATACTGCCAGTGACAAACTG	
QY	1164	GAGGAAGCGGGAGCAAGCTCAAGTCATCATGCCCTTTACGACGAGGCTACACAGTGC	1223
Db	91824		91765
		GAGGAAGCGGGAGCAAGCTCAAGTCATCATGCCCTTTACGACGAGGCTACACAGTGC	
QY	1224	TACAATGGTAGTACAGAGGGCAGCTTACACAGCGATGTGATCGGAATCTCAAAAGGCTTA	1283

## RESULT 2

RESUL 2  
US-09-745-476-1

US-09-743-478-I  
: Sequence 1, Application US/09745476

; sequence 1, Application US  
; Patent No. US20010029039A1

; PATENT NO. US2001002  
; GENERAL INFORMATION:  
; GENERAL INFORMATION:

GENERAL INFORMATION: CANON INC.

APPLICANT: CANON INC.  
TITLE OF INVENTION: Preparation of Poly-hydroxyalkanoic Acid

; TITLE OF INVENTION: FPG  
 : FILE REFERENCE: 4351008

FILE REFERENCE: 4351008  
CURRENT APPLICATION NUMBER: IIS/09/745.476

;; CURRENT APPLICATION NUMBER: US/09/145,476  
: CURRENT FILING DATE: 2000-12-26

: CURRENT FILING DATE: 20  
 : NUMBER OF SEQ ID NOS: 1

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; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word

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; SOFTWARE: MI
: SEQ ID NO 1

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; SEQ ID NO 1
: LENGTH: 1501
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; LENGTH: 1501
; TYPE: DNA

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; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens Pf0-1 . EPPM D-17445

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; ORGANISM: P  
HIS-09-74E-176-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;

Query Match 100%; Score 100%; DB 3  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
72.0%;

BEST LOCAL SIMILARITY 83.9%; FREQ. NO: 1.2E-288;  
 Mismatches 0: Mismatches 202: Indels 9: Gaps 6:

30 GGCGGCAGGCTTAACACATGCAGTCGAGCGGAAACGATGATAGCTTGTCTATTAGGCGTC 89

QY 30 GGCACAGGCTATACACATGCATGCTCGACCGATACGATGCTATAGGGCTC 69

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QY 90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGATAGCTCGG 149

Db 67 G---CGGCGACGGTGAGTAATGCCCTAGGAATCTGCCCTGGTAGTGGGGACAACGTCTC 123

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[illegible]

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Db 244 ACGATCCGTAAC TGGTCTGAGAGGATGATCAGTCACACTGGAAC TGAACACGTC CAGA 303

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QY 1444 TCATGACTGGGTTAAGTCTGACCAAGGTAGCCGTAGGGGAACCTTGGGCTGGATCAC 1501  
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RESULT 3  
US-09-821-016-5  
; Sequence 5, Application US/09821016  
; Patent No. US20010046692A1  
; GENERAL INFORMATION:  
; APPLICANT: CANON INC.  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 4051021  
; CURRENT APPLICATION NUMBER: US/09/821,016  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii P161; BP-7376  
; FEATURE:  
US-09-821-016-5

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
QY 30 GCGGCGAGGCTTAACACATGCAAGTCGAGCGGAAACGATAGATGCTTCTATTAGCGTC 89  
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QY 90 GAGCNGCGGAGCGGTGAGTAACTATTAGGAATCTACCTAGTGTGGGGATAGCTCGGG 149  
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Db 364 GCCCGGTGTGTAAGAGGCGCTTTTGGTTGTAAGCACTTTTAAAGCACTTTTAAAGCACT 423  
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Db 424 TAACTTAATACGTTAGTGTGTTGAGCTTTACCGACAGAAATAGCAGCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCGCGTAAATACAGAGGTCGAAGGTTTAAATCGGAATTTACTGGGCGTAAAGCGA 567  
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QY 688 CGTAGATCTGAAGGAATACCGATGCGAAGGAGGCTTCTTGGCATCATACTGACACTG 747  
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Db 1024 CTGTCTGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGACAGAGCGCAACCTTGT 1083
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## RESULT 4

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US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. US200202253A1
; GENERAL INFORMATION:
; APPLICANT: Caron Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate its manufacturing method, and microorganism
; TITLE OF INVENTION: those are used for the method.
; FILE REFERENCE: 4351009
; CURRENT APPLICATION NUMBER: US/09/748,205
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1
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Query Match 72.08; Score 1098.6; DB 9; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;
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Qy 30 GGCGGACGGCTTAAACATGTCGAAGTCGAGCGGAAACGATGATAGCTTGTCTATTAGCGCTC 89
Db 9 GGCGGACGGCTTAAACATGTCGAAGTCGAGCGG--ATGACGGGAGCTTGTCTCTGAATTCA 66
Qy 90 GAGCNGCGGACGGGTGAGTAATACCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGGG 149
Db 67 G---CGCGGACGGGTGAGTAATGCTTCCCTAGGAATCTGCTGTAGTGGGGACACGCTCTC 123
Qy 150 GAAACTCGAATTAATAACCGCATACGT-CTACGGGAGAAACGAGGGGNTCAATTAGACCTTG 208
Db 124 GAAAGGACGCTAATACCGCATACGTCTACGGGAGAAACGAGGGACCTTCGGGCGCTTG 183
Qy 209 CGCTATTAGATGACCTTAAGTCGATAGTACGATGGTGGGTAAAGGCTTACCATGGCG 268
Db 184 CGCTATTAGATGACCTTAAGTCGATAGTACGATGGTGGGTAAAGGCTTACCATGGCG 243
Qy 269 ACCATCTGTAGCTGGTCTGAGAGGATGATCAGGCACACCGGGACTGAGACACGGCCCGGA 328
Db 244 ACATTCGTTAACTGGTCTGAGAGGATGATCAGTCACTGGAACCTGAGACACGGTCCAGA 303
Qy 329 CT-CTACGGGAGGACGACGATGGGGAATATTGGAACAATGNGGGAACCTTGATCCAGCCAT 387
Db 304 CTCTACGGGAGGACGACGATGGGGAATATTGGAACAATGGCGGAAGCTGATCCAGCCAT 363
Qy 388 GCCGCTGTGTGAGGAAGGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAGACTCT 447
Db 364 GCCGCTGTGTGAGGAAGGCTTTTGGGATTTGTAAGCACTTTAAGTTGGGAGGAGGCGAT 423
Qy 448 TCGTTTAAATACCCGGGACGATGACATTAAGTCTGAGAAATAGCACCGGCTAACTCTGTGC 507
Db 424 TAACCTTAATACGTTAGTGTGTTGACCTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483
Qy 508 CAGCAGCGCGGTAAATACAGAGGTCGAAAGCGTTAATTCGGAATTACTGGCGTTAAAGCGA 567
Db 484 CAGCAGCGCGGTAAATACAGAGGTCGAAAGCGTTAATTCGGAATTACTGGCGTTAAAGCGC 543
Qy 568 GCGTAGTGTGTGATAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 627
Db 544 GCGTAGTGTGTGATAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 603
Qy 628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGAAAGTAGAATTTCAAGGTGTAGCGGTGAAATG 687
Db 604 AAACTGACAACTAGAGTATGTTAGAGGTTGTTGAAATTTCTCTGTGTAGCGGTGAAATG 663
Qy 688 CGTAGAGATCTGAGGAATACCGATGGCGAAGGACGCTTCTGGCATCATACTGACACTG 747
Db 664 CGTAGATATAGGAAGGAACCAAGTGGCGAAGGCGAACCTCTGGACTGATCTGACACTG 723
Qy 748 AGGTGCAAGCGTGGGTAGCAAAACAGGATTAGATACCTCTGGTAGTCCACCGCTAAACG 807
Db 724 AGGTGCAAGCGTGGGTAGCAAAACAGGATTAGATACCTCTGGTAGTCCACCGCTAAACG 783
Qy 808 ATGTCTACTAGTGTGGTTCCTTGAGGACTTGTAGGACGCTTACGCACTAACGCAATTAAGTAGA 867
Db 784 ATGTCAACTAGCGTTGGGAGCCTTGAGCTCTTAGTGGCGAGCTAACGCAATTAAGTTGA 843
Qy 868 CCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTAAGGAGGAGGCGGCGGCGCAAA 927
Db 844 CCGCTGGGAGTACGGCCGCAAGTTAAACTCAATGAATTAAGGAGGAGGCGGCGGCGGCGCAAA 903
Qy 928 GCGGTGGAGCATGTGGTTTAAATTCGATGCAACGCGGAAGAACTTACCTGGTCTTGTACATA 987
Db 904 GCGGTGGAGCATGTGGTTTAAATTCGAGCAACGCGGAGAACCTTACCAGGCGCTTGACATC 963
Qy 988 CACAGAACTTTGTAGAGATACGAGAGTGCCTTCGGGAAATTTGTGATACAGGTGCTGCATGG 1047
Db 964 CAATGAACTTTCCAGAGATGAGTGGTGCCTTCGGGAAACATTTAGACAGGTGCTGCATGG 1023
Qy 1048 CTGTCTGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1107
Db 1024 CTGTCTGTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1083
```



QY 1108 CCTTAGTTACAGCAC-ITTCGGGTGGGAACTCTAAAGGATATGCGAGTACAAAATGGAG 1166  
Db |||||  
1084 CCTTAGTTACAGCACGTAATGGTGGCACTCTAAAGGAGACTGCCGGTGACAAAACGGAG 1143  
QY 1167 GAAGCGGGGACAGCTCAAGTCATCATGCGCCCTTACGACAGGCTACACAGTGTCTAC 1226  
Db |||||  
1144 GAAGGTGGGGATGAGCTCAAGTCATCATGCGCCCTTACGGCCCTGAGGCTACACAGTGTCTAC 1203  
QY 1227 AATGTTAGTACAGAGGGCAGCTACACAGCGATGTGATCGGAATCTCAAAAAGCCATCG 1286  
Db |||||  
1204 AATGTTAGTACAGAGGGTTCGCAAGCCGAGAGTGGAGCTAATCCACAAAACCGATCG 1263  
QY 1287 TAGTCCAGATGAGGCTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346  
Db |||||  
1264 TAGTCCGATCGAGTCTGCAACTCGACTCGCTGAAGTCGGAATCGCTAGTAATCGCGAA 1323  
QY 1347 TCAGAAATGCGCGGTGAATACCTTCCCGGCCCTGTACACACCGCCCGTACACCATGGG 1406  
Db |||||  
1324 TCAGAAATGTCGGGTGAATACCTTCCCGGCCCTGTACACACCGCCCGTACACCATGGG 1383  
QY 1407 AGTTGATTGCACAGAGGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACACGGTGTGT 1465  
Db |||||  
1384 AGTGGTTGCACAGAGTAGTCTTAACCTTCGGGAGGAGCTTACCACGGTGTGTAT 1443  
QY 1466 CGATGACTGGGTGAAGTCGTAAAGGTAGCCGTAGGGAACCTGCGGCTGGATCAC 1523  
Db |||||  
1444 TCATGACTGGGTGAAGTCGTAAAGGTAGCCGTAGGGAACCTGCGGCTGGATCAC 1501

RESULT 5  
US-09-793-920A-1  
; Sequence 1, Application US/09793920A  
; Patent No. US20020065389A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as  
; FILE OF INVENTION: monomer unit, and method for producing the same.  
; FILE REFERENCE: 4396021  
; CURRENT APPLICATION NUMBER: US/09/793,920A  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain.  
US-09-793-920A-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTCTATTAGCGCTC 89  
Db |||||  
9 GCGCGAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGAGCTTGTCTCTGAATTCA 66  
QY 90 GAGCNCGGGACGGGTGAGTAATCTTAGGAATCTTACCTAGTAGTGGGGGATAGCTCGG 149  
Db |||||  
67 G---CGGCGACGGGTGAGTAATGCTTAGGAATCTGCTGTGTAGTGGGGACAACTCTC 123  
QY 150 GAACTCGAATTAATACCGCATACCT-CTACGGGAGAAAGCAGGGGNTCATTTAGACCTTG 208  
Db |||||  
124 GAAAGGAGCGCTTAATACCGCATACCTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
QY 209 CGCTATTAGTCAGCTTAAGTCGGATAGCTAGTAGTGGGTAAAGCCCTACCATGGG 268  
Db |||||  
184 CGCTATTAGTCAGCTTAAGTCGGATAGCTAGTGGGTAAAGCCCTACCATGGG 243  
QY 269 ACATCTGTAGTGTCTGAGAGGATGATCAGCCACACGGGACTGAGACAGCGGCCGA 328  
Db |||||  
244 ACATCCGTAACTGTCTGAGAGGATGATCAGTCACTGTGNACTGAGACACGGTCCAGA 303  
QY 329 CT-CTACGGGAGGACAGTGGGGAATATTGGACAATGNGGGAACCTCGATCCAGCAT 387  
Db |||||

Db 304 CTCCTACGGGAGGACGAGTGGGGAATATTGGACAATGGCGAAAGCCTGATCCAGCCAT 363  
QY 388 GCGCGTGTGTCAAGAGCGCTTTTGGTTGTAAAGCACTTTTAAAGCAGTGAAGAAGCACTCT 447  
Db 364 GCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTTAAAGTGGAGGAAGGGAT 423  
QY 448 TCGGTTAATACCCGGGACGATGACATTTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACTTAATACGTTAGTGTGAGCTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCGGCGTAAAGCGC 543  
QY 568 CGTAGTGGCTTGATAGTCAAGTGTGAAATCCCGGGCTTAACTCGGAACTGCATCT 627  
Db 544 CGTAGTGGCTTGATAGTGTGAAATCGGAGTGTGAAAGCCCGGCTCAACTCGGAACTGCATCT 603  
QY 628 GAACTGTGTTAGCTAGTGTGAGAGGAGTAGAATTTTCAAGTGTAGCGGTGAATG 687  
Db 604 AAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGAATTTTCTGTGTAGCGGTGAATG 663  
QY 688 CGTAGATCTGAAGGAATACCGATGCGGAAGGAGCTTCTTGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACAGTGGCGAAGGAGCACCTGGACTGATTAATGACACTG 723  
QY 748 AGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCTGTAGTGCACGCGTAAACG 807  
Db 724 AGTGGGAAGCGTGGGAGCAACAGGATTAGATACCTGTGTAGTGCACGCGGTAAACG 783  
QY 808 ATGTCTACTAGTGTGGTCCCTTGGAGCACTTAGTGACGCGAGCTTAACGCAATAGTAGA 867  
Db 784 ATGTCAACTAGTGTGGGAGCTTTGAGCTCTTAGTGGCGAGCTTAACGCAATAGTAGA 843  
QY 868 CCGCTCGGAGTAGCGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCACAA 927  
Db 844 CCGCTCGGAGTAGCGCGCAAGGTTAAACTCAATGAATTAAGCGGGGCGCGCACAA 903  
QY 928 GCGGTGGAGCATGTGTTTAAATTCGATGCAACGGAAGCACTTACCTGCTTGCACATA 987  
Db 904 GCGGTGGAGCATGTGTTTAAATTCGAGCAACGGAAGCACTTACCGAGGCTTGCACATC 963  
QY 988 CACAGAACTTTGTAGAGATACGAGAGTGCCTTCGGGAATTTGTGATACAGGTGCTGCATGG 1047  
Db 964 CAATGAACCTTCCAGAGATGATGGTGCCTTCGGGAACATTTGAGACAGGTGCTGCATGG 1023  
QY 1048 CTGTCTGAGTCTGTGAGATGTGGGTAAAGTCCCGCAAGGAGCAACCCCTTGT 1107  
Db 1024 CTGTCTGAGTCTGTGAGATGTGGGTAAAGTCCCGTAAACGAGCGCAACCCCTTGT 1083  
QY 1108 CTTAGTTTACCGACAC-ITTCGGGTGGGAACCTCTAAGGATCTGCGAGTGACAAACTGGAG 1166  
Db 1084 CTTAGTTTACCGACACGTAATGTGTGGCACTCTTAGGAGACTGCGGTGACAAACCGGAG 1143  
QY 1167 GAAGCGGGGACGAGCTCAAGTCAATGCGCCCTTACGACAGGCTACACAGTGTCTAC 1226  
Db 1144 GAAGGTGGGATGACGTCAGTCACTATGCGCCCTTACGGCTTACGACAGTGTCTAC 1203  
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGCGATGTGATCGGAATCTCAAAAAGCCATCG 1286  
Db 1204 AATGTTAGTACAGAGGCTTCCAAAGCGCGAGGTGGAGCTTAATCCCAACAAACCGATCG 1263  
QY 1287 TAGTCCAGATTTGAGTCTGCAACTCGACTCAAGTGGAGTGGGTAGTAAATCGCGGA 1346  
Db 1264 TAGTCCGATCGAGTCTGCAACTCGACTGCGTGAAGTTCGGAATCGCTAGTAATCGGAA 1323  
QY 1347 TCAGAAATGCGCGGTGAATAGCTTCCGGGCTTGTACACACCGCCCGTCAACCATGGG 1406  
Db 1324 TCAGAAATGCGCGGTGAATAGCTTCCGGGCTTGTACACACCGCCCGTCAACCATGGG 1383  
QY 1407 AGTTGATTGACAGAGAGTGGTTAGCCTAA-CTTAGTGAGGCGGATCAACAGGTTGGT 1465  
Db 1384 AGTGGTTGACAGAGAGTGGTTAGCCTAACTTTCGGGAGGAGCGGTTACCGGTTGTAT 1443

QY 1466 CGATGACTGGGGTGAAGTCCTAAACAGGTAGCCGTAGGGAAACCTGGCGCTGGATCAC 1523  
Db 1444 TCATGCTGGGGTGAAGTCCTAACCAAGTAGCCGTAGGGAAACCTGGCGCTGGATCAC 1501

## RESULT 6

US-09-951-720-1  
; Sequence 1, Application US/09951720  
; Patent No. US20020160467A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Kabushiki Kaisha  
; TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof  
; FILE REFERENCE: 4477001  
; CURRENT APPLICATION NUMBER: US/09/951,720  
; PRIOR FILING DATE: 2000-09-14  
; JP 378827/2000  
; JP 165238/2001  
; JP 165509/2001  
; JP 275063/2001  
; PRIOR FILING DATE: 2000-09-14  
; 2000-12-13  
; 2001-05-31  
; 2001-09-11  
; 2001-09-11  
; NUMBER OF SEQ ID NOS: 1  
; SEQ ID NO 1  
; TYPE: DNA  
; LENGTH: 1501  
; ORGANISM: Pseudomonas jessenii P161 strain.  
US-09-951-720-1

Query Match 72.0%; Score 1098.6; DB 9; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGAGGCTTAACACATGCAAGTCGAGCGGAACCATGATGACTTGTCTATTAGCGTC 89  
Db 9 GCGCGAGGCTTAACACATGCAAGTCGAGCGG--ATGCGGAGCTTGTCTCTGAATCA 66  
QY 90 GAGNCGCGGACGGGTGAGTAATCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGG 149  
Db 67 G---CGGCGGACGGGTGAGTAATGCTTAGGAATCTGCTGTGTAGTGGGGACACGTC 123  
QY 150 GAACTCGAATTAATACCGCATAGT-CTACGGAGAAAGCAGGGGNTCAATGACCTTG 208  
Db 124 GAAAGGGACGCTAATACCGCATAGTCTTACGGGAGAAAGCAGGGGACCTTTCGGGCTTG 183  
QY 209 CGCTATTAGATGAGCTAAGTCGATAGTATGTTGGGTAAAGGCTTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCTTAGTTCGATAGTATGTTGGGTAAAGGCTTACCATGGCG 243  
QY 269 ACATCTGTAGCTGTCTGAGAGGATGATCAGCACACCGGAGCTGAGACACGCGCGGA 328  
Db 244 ACATCTGTAGCTGTCTGAGAGGATGATCAGTCACTGGAATCTGAGACACGCTCCAGA 303  
QY 329 CT-CTACGGGAGGACAGTGGGAATATTGGCAATATGNGGGAACCTGATCAGGCAT 387  
Db 304 CTCCTACGGGAGGACAGTGGGAATATTGGCAATATGNGGGAACCTGATCAGGCAT 363  
QY 388 GCCCGGTGTGGAAGAAGGCTTTTGTGTGTAAGCACTTTAAGCAGTGAAGAAGACTCT 447  
Db 364 GCCCGGTGTGGAAGAAGGCTTTTGTGTGTAAGCACTTTAAGTGGGAGGAGGCAT 423  
QY 448 TCGGTTAATCCCGGGACCATGATGATGCTGAGAAATAGCACCGGCTAACTCTGTGC 507  
Db 424 TAACTAATACGTTAGTGTGTTGACGTTTACCGACAGAAATAGCACCGGCTAACTCTGTGC 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTCGAAGCTTAATCGGAATTTACTGGCGGTAAAGCA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTCGAAGCTTAATCGGAATTTACTGGCGGTAAAGCGC 543

QY 568 CCGTAGTGCCTTGATAGTCAAGTCAGATGTGAATCCCGGGCTTAAACCTGGGAACGTGATCT 627  
Db 544 CCGTAGTGCCTTGTGTTAAGTGTGAAGAGCCCGGGCTCAACCTGGGAACGTGATTC 603  
QY 628 GAAACTGCTTAGGCTAGAGTAGGTAGAGGGAAGTAGAATTTTCAAGTGTGACGGTGAATG 687  
Db 604 AAACTGACAAGCTAGAGTATGGTAGGGTGTGGAATTTCTGTGTAGCGGTGAATG 663  
QY 688 CGTAGAGATCTGAAGGAATACCATGGCGAAGCAGCTTCTCTGGCATCATCTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACCAAGTGGCGAAGCGCACCTCTGGAATGATGACTGAC 723  
QY 748 AGCTCGAAGAGCTGGGTAGCAACAGGATAGATACCTCTGGTAGTCCACGCCGTAAACG 807  
Db 724 AGGTGCAAAAGCTGGGGAGCAAAACAGGATTAGATACCTCTGGTAGTCCACGCCGTAA 783  
QY 808 ATGCTACTAGTCTGTTGGGTCCCTTCAGGACTTAGTACGACAGCTTAACGCAATAAGTAG 867  
Db 784 ATGCTCACTAGCCGTTGGGAGCCTTGAAGCTCTTAGTGGGCGACCTAACGCAATTAAG 843  
QY 868 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTTGACGGGGGCCCGCACAA 927  
Db 844 CCGCTGGGAGTACGCGCGCAAGGTTAAACTCAATGAATTTGACGGGGGCCCGCACAA 903  
QY 928 GCGGTGGAGCATGCTGTTTAAATTCGATGCAACGCGAAGACCTTACTTGTCTTGACATA 987  
Db 904 GCGGTGGAGCATGCTGTTTAAATTCGAGCAACCGAAGAACCTTACCGAGCCTTGACATC 963  
QY 988 CACAGAACTTTGATAGATACGAGAGTGCCTTCGGGAATTTGTATACAGGTGCTGCATGG 1047  
Db 964 CAATGAATTTCCAGAGATGGATGGTGCCTTCGGGAATTTGAGACAGGTGCTGCATGG 1023  
QY 1048 CTGCTGACGCTGCTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGCTGACGCTGCTGTGAGATGTTGGGTTAAGTCCCGTAAACGAGCGCAACCTTGT 1083  
QY 1108 CCTTAGTACCAGCAC-TTCGGGTGGAACTCTTAAGGATCTGCGAGTGACAACTGGAG 1166  
Db 1084 CCTTAGTACCAGCACGTAATGTTGGGCACTCTAAGGAGACTGCCGTTGACAAACCGGAG 1143  
QY 1167 GAAAGCGGGGACGACCTCAAGTCATCATGGCCCTTACGACCGAGGGCTACACAGCTGTAC 1226  
Db 1144 GAAAGTGGGATGACCTCAAGTCATCATGGCCCTTACGGCTTGGGCTACACAGCTGTAC 1203  
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGGATGATCGGAATCTCAAAAGCCTATCG 1286  
Db 1204 AATGTTAGTACAGAGGCTTGCAGCGAGGTGCGAAGCGAGGTGAGCTAATCCCAAAACCG 1263  
QY 1287 TAGTCCAGATTTGAGTCTGCACTCGACTCCATGAAGTAGGAATCGCTAGTAAATCGCGGA 1346  
Db 1264 TAGTCCGATTCGAGTCTGCACTCGACTCGCTGAGTGGATCGGAATCGTAGTAATCGGAA 1323  
QY 1347 TCAGAAATGCGCGGTGAATACGTTCCCGGCTTGTATACACGCGCGCTACACCATGGG 1406  
Db 1324 TCAGAAATGCGCGGTGAATACGTTCCCGGCTTGTATACACGCGCGCTACACCATGGG 1383  
QY 1407 AGTTGATTCACAGAGTGGTTAGCTTAA-CTTAGTGGGGGATGATCAACCGGTGTGT 1465  
Db 1384 AGTGGTTTCACAGAGTGGTTAGCTTAACTTCCGGAGGACGGTTACACCGGTGTGT 1443  
QY 1466 CGATGACTGGGTGAAGTCTGAACAGGTAGCGGTAGGGGAACCTCGCGCTGGATCAC 1523  
Db 1444 TCATGACTGGGTGAAGTCTGTACCAAGTGTAGCGGTAGGGGAACCTCGCGCTGGATCAC 1501

## RESULT 7

US-09-791-610-1  
; Sequence 1, Application US/09791610  
; Publication No. US20030100084A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid as  
; monomer unit, and method for producing the same.

Qy	928	GC	GTGGAGCATGTGGTTTAAATTCGATGCAACCGGAAGAACTTTACCTGTGTTGACATA	987
Db	904	GC	GTGGAGCATGTGGTTTAAATTCGAAGCAACGCGAAGAACCTTTACCGGCTTGACATC	963
Qy	988	CAC	GAATCTTGTAGAGATACGAGAGTGCCTTCGGGNAATTTGTATACAGGTGCTGCATGG	1047
Db	964	CAATGA	AACTTTCCAGAGATGGATGGGTGCCCTTCGGGAACAATTGAGACAGGTGCTGCATGG	1023
Qy	1048	CTGT	CGTCAGCTCGTGTGCGTAGATGTGGGTTAAAGTCCCGCAACGAGCGCAACCCCTTGT	1107
Db	1024	CTGT	CGTCAGCTCGTGTGCGTAGATGTGGGTTAAAGTCCCGTAACGAGCGCAACCCCTTGT	1083
Qy	1108	CCTTAG	TTACCAAGAC-TTCGGGTGGAACTCTTAAGGATACTGCCAGTGACAAACCTGGAG	1166
Db	1084	CCTTAG	TTACCAAGACCTAATGCTGGGCACTCTTAAGGAGACTGCGGTTGACAAACCGGAG	1143
Qy	1167	GAAG	CGGGGACACAGCTCAAGTCAATCATGCGCCCTTAGCIACAGGGCTACACAGTGTCTAC	1226
Db	1144	GAAG	GTGGGATGACGTCAGTCAATCATGCGCCCTTAGCGCTTACCGCTACACAGTGTCTAC	1203
Qy	1227	AATG	TGAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG	1286
Db	1204	AATG	TGTCGGTACAGAGGTTGCCAAGCGGAGGTGGAGCTAATCCACAAAACCGATCG	1263
Qy	1287	TAGT	CCAGATTGCGAGTCTGCAACTCGACTCCATGAAAGTAGGAATCGCTAGTAATCGCGGA	1346
Db	1264	TAGT	CCGGATCGCAGTCTGCAACTCGACTTCGCTGAAGTCGGAATCGCTAGTAATCGCGAA	1323
Qy	1347	TCAGA	TGCGCGGTGAATACGTTCCGGGCTTTGTACACACGCGCGGTACACACCATGGG	1406
Db	1324	TCAGA	TGTGCGCGTGAATACGTTCCCGGGCTTTGTACACACGCGCGGTACACACCATGGG	1383
Qy	1407	AGTT	GATTGACACAGAAAGTGGTTAGGCTAA-CTTAGTGAGGGCGATCCACCACGGTGTGGT	1465
Db	1384	AGT	GGTTCACACAGAGTAGCTAGTCTTAACCTTCGGAGAGCGGTTACCGCGTGTGAT	1443
Qy	1466	CGAT	GACTGGGGTGAAGTCGTAAACAAGTAGCGGTAGGGGAACCTGCGGCTGGATCAC	1523
Db	1444	TCAT	GACTGGGTGAAGTCGTACCAAGTAGCGGTAGGGGAACCTGCGGCTGGATCAC	1501
RESULT 8				
US-10-218-519-5				
; Sequence 5, Application US/10218519				
; Publication No. US20030049806A1				
; GENERAL INFORMATION:				
; APPLICANT: Yano, Tetsuya				
; APPLICANT: Imamura, Takeshi				
; APPLICANT: Suda, Sakae				
; APPLICANT: Honma, Teutomo				
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same				
; FILE REFERENCE: 03500.015225.1				
; CURRENT APPLICATION NUMBER: US/10/218,519				
; CURRENT FILING DATE: 2001-03-30				
; PRIOR APPLICATION NUMBER: 09/821,016				
; PRIOR FILING DATE: 2001-03-30				
; NUMBER OF SEQ ID NOS: 11				
; SOFTWARE: Microsoft Word				
; SEQ ID NO 5				
; LENGTH: 1501				
; TYPE: DNA				
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376				
; FEATURE:				
; FEATURE: cDNA to 16S rRNA				
US-10-218-519-5				
Query Match 72.0%; Score 1098.6; DB 14; Length 1501;				
Best Local Similarity 85.9%; Pred. No. 1-2e-288;				
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;				
Qy	30	GG	CGGCGAGGCTTAACATGCAAGTCAGCGGAACGATGATAGCTTGTATTAGGCGTC	89

Db 9 GGGCGGAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTCTGAATTCA 66  
Qy 90 GAGNCGCGGACGGGTGAGTAATACCTTAGTAATCTACCTAGTAGTGGGGATAGCTCGGG 149  
Db 67 G---CGCGGACGGGTGAGTAATGCTTGAAGTAATGCTGCTGTTAGTGGGGGACAACTGTC 123  
Qy 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCAATTAGACTTGG 208  
Db 124 GAAAGGACGCTAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
Qy 209 CGCTATTAGATGACCTTAAGTCGGAATTTAGTGGGTAAAGCCCTACATGGCG 268  
Db 184 CGCTATCAGATGACCTTAGCTCGGATTTAGTGGTGAAGTAAATGGCTCACCAAGGCG 243  
Qy 269 ACGATCTGTAGTGGTCTGAGAGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328  
Db 244 ACGATCCGTAACCTGCTGAGAGATGATCAGTCACACTGGAATGAGACACGGTCCAGA 303  
Qy 329 CT-CTACGGGAGGACAGTGGGGAATTTGGACAATGNGGGAACCCCTGATCCAGCCAT 387  
Db 304 CTCTACGGGAGGACAGTGGGGAATTTGGACAATGNGGGAAGGCTGATCCAGCCAT 363  
Qy 388 GCGCGTGTGTGAAGAAGGCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447  
Db 364 GCGCGTGTGTGAAGAAGGCTTTTGGATTTGTAAGCACTTTAAGTTGGGAGGAAGGCAT 423  
Qy 448 TCGGTTAATACCGGGACAGTACATTTAGCTGCAGTAATAGCACCGGCTAATCTGTGC 507  
Db 424 TAACCTAATACGTTAGTGTGTTGACGTTTACCGACAGAAATAGCACCGGCTAATCTGTGC 483  
Qy 508 CAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTTAAATCGGAATTTACTGGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGCTGCAAGCGTTTAAATCGGAATTTACTGGGCGTAAAGCGC 543  
Qy 568 GCGTAGTGGCTTGATAGTCAAGTGAATGTAATCCCGGGCTTAACTGGGAATGCAATCT 627  
Db 544 GCGTAGTGGCTTGATAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 603  
Qy 628 GAACTGTAGCTAGTGGTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 687  
Db 604 AAAACTGACAGCTAGTGGTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGCGAAGGAGCTTCTGCGCATCATCTGACACTG 747  
Db 664 CGTAGATATAGGAAGAACACCACTGCGGAAGGAGCCACCTGCACTGATGACACTG 723  
Qy 748 AGGCTGAAAGCGTGGGTAGCAAAACAGATTAAGTACCTGGTGTAGTCCACCGCGTAAACG 807  
Db 724 AGGTGCAAAAGCGTGGGAGCAAAACAGATTAAGTACCTGGTGTAGTCCACCGCGTAAACG 783  
Qy 808 ATGTCTACTAGTCCGTTGGTCCCTTGGAGACTTGTAGTCAGCAGCTAACGCAATAAGTAGA 867  
Db 784 ATGTCAACTAGCTGTTGGAGCCTTGTAGCTTTAGTGGCAGCAGTAAACGATTAAGTTGA 843  
Qy 868 CCGCTCGGGAGTACGGCGCAAGGTTAAATCTCAAAATGAATGACGGGGCCCGCACAA 927  
Db 844 CCGCTCGGGAGTACGGCGCAAGGTTAAATCTCAAAATGAATGACGGGGCCCGCACAA 903  
Qy 928 GCGGTGAGCATGTGTTTAAATTCGATGCAACGGGAAGAACCTTACCTGGTCTTGACATA 987  
Db 904 GCGGTGAGCATGTGTTTAAATTCGAAAGCAACGGGAAGAACCTTACCGAGGCTTTGACATC 963  
Qy 988 CACAGAACTTTGTAGAGATACGAGGTCCCTTGGGAAATTTGTATACAGGTGCTGCAATGG 1047  
Db 964 CAATGAATTTCCAGAGATGATGGTGGCTTCCGGGAACATTTGAGACAGGTGCTGCAATGG 1023  
Qy 1048 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTTGT 1107  
Db 1024 CTGTCTGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGTAAACGAGCGCAACCTTTGT 1083  
Qy 1108 CTTAGTTACAGAC--TTCCGGGTGGGAACCTTAAGGATGACTGCACTGACAACTGGAG 1166  
Db 1084 CTTAGTTACAGACCGTAATGGTGGGCACTCTAAGGAGACTGCGCGGTGACAAACCGGAG 1143

Qy 1167 GAAGCGGGGACGACGCTCAAGTCAATCATGCGCCCTTACGACACGAGGCTTACACAGTGTCTAC 1226  
Db 1144 GAAGTGGGGATGACGCTCAAGTCAATCATGCGCCCTTACGCGCTGGGCTACACAGTGTCTAC 1203  
Qy 1227 AATGTAGGTACAGAGGGGAGCTTACACAGCATGTGATCGAATCTCAAAAAAGCCTATCG 1286  
Db 1204 AATGTGCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCACAAACCGATCG 1263  
Qy 1287 TAGTCCAGATTTGGAGTCTGCAACTCGACTCCATGAATAGGATCGTAGTAAATCGGGA 1346  
Db 1264 TAGTCCGGAATCGCAGTCTGCAACTCGACTCCGTAAGTGGAAATCGTAGTAAATCGGGA 1323  
Qy 1347 TCAGAAATCGCGGCTGAATACGTTCCCGGCGCTTTGTACACACCGCCCGTACACACCATGGG 1406  
Db 1324 TCAGAAATGTCGCGGTGAATACGTTCCCGGCGCTTTGTACACACCGCCCGTACACACCATGG 1383  
Qy 1407 AGTTGATTCACACAGAAAGTGGTTAGCTAA-CTTAGTGAGGGCGATCAACGAGTGTGGT 1465  
Db 1384 AGTGGGTTGCACCAGAAAGTAGCTAGTCTAACTTCGGGAGGACGGTTACACGCTGTAT 1443  
Qy 1466 CAGTACTGGGCTGAAGTCTGAACAGGTAGCGGTAGGGGACCTGGGCTGGATCAC 1523  
Db 1444 TCATGCTGGGCTGAAGTCTGTAACAGGTAGCGGTAGGGGAACTCGGCTGGATCAC 1501

RESULT 9  
US-10-266-787-5  
; Sequence 5, Application US/10286787  
; Publication No. US20030082777A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Tetsuya  
; APPLICANT: Imamura, Takeshi  
; APPLICANT: Suda, Sakae  
; APPLICANT: Honma, Tsutomu  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 03500.015225.3  
; CURRENT APPLICATION NUMBER: US/10/266,787  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: JP 2000-095004  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376  
; FEATURE:  
; FEATURE: cDNA to 16S rRNA  
US-10-266-787-5

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;  
Best Local Similarity 85.9%; Pred.No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
Qy 30 GCGCGCAGGCTTAACACATGCAAGTGCAGCGAAACGATGATGCTTGTATAGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATGCAAGTGCAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66  
Qy 90 GAGNCGCGGACGGGTGAGTAATACCTTAGTAATCTACCTAGTAGTGGGGATAGCTCGGG 149  
Db 67 G---CGCGGACGGGTGAGTAATGCTTGAAGTAATGCTGCTGTTAGTGGGGGACAACTGTC 123  
Qy 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCAATTAGACTTGG 208  
Db 124 GAAAGGACGCTAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
Qy 209 CGCTATTAGATGACCTTAAGTCGGAATTTAGTGGGTAAAGCCCTACATGGCG 268  
Db 184 CGCTATCAGATGACCTTAGCTCGGATTTAGTGGTGAAGTAAATGGCTCACCAAGGCG 243  
Qy 269 ACGATCTGTAGTGGTCTGAGAGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db 244 ACGATCCGTAACGTGCTGAGAGGATGATCACTGCACTGGAACCTGAGACACGGTCCAGA 303  
QY 329 CT-CTACGGAGGACGACGTGGGGAATATTGGACAATGNGGGAACCCCTGATCCAGCCAT 387  
Db 304 CTCCTACGGAGGACGACGTGGGGAATATTGGACAATGNGGGAACCCCTGATCCAGCCAT 363  
QY 388 GCCCGGTGTGTGAAGAAGCCCTTTTGGTGTAAAGCAGCTTTAAAGCAGTGAAGAAGACTCT 447  
Db 364 GCCCGGTGTGTGAAGAAGCTCTCGGATTTGTAAGCAGCTTTAAAGTGGGAGGAGGCAT 423  
QY 448 TCGGTTAATACCCGGGACGATGACATTAGCTGCGAATAAGCAGCGCTAATCTGTGCG 507  
Db 424 TAACCTAATACCTTGTAGTTGCTTACCCAGACAATAAGCAGCGCTAATCTGTGCG 483  
QY 508 CAGCAGCCGCGTAATACAGAGGCTGCAAGCGCTTAATCGGAATTAATCTGGGCGTAAAGCGA 567  
Db 484 CAGCAGCCGCGTAATACAGAGGCTGCAAGCGCTTAATCGGAATTAATCTGGGCGTAAAGCGC 543  
QY 568 GCGTAGGTGGTGTGATAAGTCAAGTGTGAAATCCCGGGCTTAACTGGGAACTGCAATCT 627  
Db 544 GCGTAGGTGGTGTGATAAGTGTGAAATCCCGGGCTTAACTGGGAACTGCAATCT 603  
QY 628 GAAACTGTTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 687  
Db 604 AAAAATGCAAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 663  
QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGCGAGCTTCTCGGCATCATCTGACACTG 747  
Db 664 CGTAGATATAGAAGGAACACAGTGGCGAAGCGAGCTTCTCGGCATCATCTGACACTG 723  
QY 748 AGGCTGGAAGCGTGGGTAGCAAAACAGGATTAATACCTGGTGTAGCTAGCTAGCTAGCTAGCT 807  
Db 724 AGGCTGGAAGCGTGGGTAGCAAAACAGGATTAATACCTGGTGTAGCTAGCTAGCTAGCTAGCT 783  
QY 808 ATGCTACTAGCTGGTGGTCCCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 867  
Db 784 ATGCTACTAGCTGGTGGTCCCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCT 843  
QY 868 CGGCTCGGGAGTACGGCGCAAGGTAAAGCTCAAACTGAAATGAAATGAAATGAAATGAAATGAA 927  
Db 844 CGGCTCGGGAGTACGGCGCAAGGTAAAGCTCAAACTGAAATGAAATGAAATGAAATGAAATGAA 903  
QY 928 GCGGTGGAGCATGTGGTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987  
Db 904 GCGGTGGAGCATGTGGTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 963  
QY 988 CACAGATCTGTAGAGATACAGAGTGGCTTCGGGAATTTGATACAGGTGCTGCTATGG 1047  
Db 964 CAATGAACTTTCAGAGATGGATGGGTGCTTTCGGGAACATTTGAGACAGGTGCTGCTATGG 1023  
QY 1048 CTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGAACCCTTGT 1107  
Db 1024 CTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGTAACGAGCGCAACCCTTGT 1083  
QY 1108 CTTTAGTTACCAAGCAC-TTCGGGTGGGAACCTTAAGGATACCTGCGAGTGACAAACCTGGAG 1166  
Db 1084 CTTTAGTTACCAAGCACGTAATGTTGGGCACCTTAAGGAGACTGCGGGTGACAAACCTGGAG 1143  
QY 1167 GAAGCGGGGACGAGCTCAAGTCAATGCGCCCTTACGACAGGCTTACACAGGTGCTAC 1226  
Db 1144 GAAGGTGGGGATGAGCTCAAGTCAATGCGCCCTTACGCGCTTACGCGCTTACGCGCTTACGCGCT 1203  
QY 1227 AATGTTAGTACAGAGGCGAGCTACACAGCGATGTTGATGCGAATCTCAAAAGCCCTATCG 1286  
Db 1204 AATGTTAGTACAGAGGCTTGGCAAGCGCGAGGTGGAGCTAATCCCAAAACCGATCG 1263  
QY 1287 TAGTCCAGATTGAGCTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCCGGGA 1346  
Db 1264 TAGTCCGAGTCTGCAACTCGACTCGCTGGAAGTCCGGAATCGCTAGTAATCCGGGA 1323  
QY 1347 TCAGAAATCCCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCACACCATGG 1406  
Db 1324 TCAGAAATGTCGGGTGAATACGTTCCCGGGCTTGTACACACCGCCGCTCACACCATGG 1383

QY 1407 AGTTGATTGCCAGGAAGTGGTTAGCCTAA-CTTAGTGAGGCGGATCACCACGGTGTGGT 1465  
Db 1384 AGTGGTTGCCACGAGAGTAGTACTAGCTTAACTTCGGAGGACGGTTACCACGGTGTGAT 1443  
QY 1466 CGATGACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGGAACCTTCGGGCTGGATCAC 1523  
Db 1444 TCATGACTGGGGTGAAGTCGTAAACAGGTAGCCGTAGGGGAACCTTCGGGCTGGATCAC 1501

## RESULT 10

US-10-252-518-5  
; Sequence 5, Application US/10252518  
; Publication No. US20030087413A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Tetsuya  
; APPLICANT: Imamura, Takeshi  
; APPLICANT: Suda, Sakae  
; APPLICANT: Honma, Tsutomu  
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme  
; FILE REFERENCE: 03500.015225.2  
; CURRENT APPLICATION NUMBER: US/10/252,518  
; CURRENT FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: JP 2000-095004  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 5  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii Pl61 ; BP-7376  
; FEATURE:  
; FEATURE: cDNA to 16S rRNA  
US-10-252-518-5

Query Match 72.0%; Score 1098.6; DB 14; Length 1501;

Best Local Similarity 85.9%; Pred. No. 1.2e-288;

Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

QY 30 GCGCGCAGGCTTAACACATGCAAGTCGAGCGGAACGATGATAGCTTCTTATAGGCGTC 89  
Db 9 GCGCGCAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTGAAATCA 66  
QY 90 GAGCNGCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149  
Db 67 G---CGCGGACGGGTGAGTAATGCCTAGGAATCTGCTGTGTAGTGGGGGACAGCTCTC 123  
QY 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTTAGACCTTG 208  
Db 124 GAAAGGACGCTAATACCGCATACGTCTACGGGAGAAAGCAGGGGACCTTCGGGCTTG 183  
QY 209 CGCTATTAGATGCGCTTAAGTCGGATTAGCTAGATGGTGGGTAAGCCCTACCATGGCG 268  
Db 184 CGCTATCAGATGAGCCCTAGGTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 243  
QY 269 ACAGTCTGTAGCTGCTGAGAGGATGATCAGCACACCGGAGCTGAGACACGGCCCGGA 328  
Db 244 ACAGTCCGTAATGCTGCTGAGAGGATGATCAGTCACTGGAATGAGACACGGTCCAGA 303  
QY 329 CT-CTACGGGAGGACGAGTGGGGAATTTGGCAAAATGNGNGGAACCTTGATCCAGCCAT 387  
Db 304 CTCCTACGGGAGGACGAGTGGGGAATTTGGCAAAATGNGNGGAACCTTGATCCAGCCAT 363  
QY 388 GCCCGGTGTGTGAAGAAGCCCTTTTGGTTGTAAGCACTTTTAAAGCTGGAAGAGACTCT 447  
Db 364 GCCCGGTGTGTGAAGAAGCTCTTCGGATTGTAAGCACTTTTAAAGCTGGAAGAGAGGCAAT 423  
QY 448 TCGGTTAATACCCGGGACGAGTACATAGCTGAGAAATAAGCACCGGCTAACTCTGTGCG 507  
Db 424 TAACCTAATACGTTAGTGTGTTGAGCTTTACCGACAGAATAAGCACCGGCTAACTCTGTGCG 483  
QY 508 CAGCAGCGCGGTAAATACAGAGGTGCAAGCGTTAATCGGAATTAATCTGGGCGTAAAGCGA 567





Db 784 ATGTCAACTAGCGTGTGGAGCCTTACGCTCTAGTGGCGAGCTAAACGCAATTAAGTTGA 843  
Qy 868 CCGCTCTGGGAGTACGGCGCAAGGTTAAATCAAAATCAATTAAGTGGGCGCCGCAAA 927  
Db 844 CCGCTCTGGGAGTACGGCGCAAGGTTAAATCAAAATCAATTAAGTGGGCGCCGCAAA 903  
Qy 928 GCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987  
Db 904 GCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATC 963  
Qy 988 CACAGAACTTTAGAGATACAGAGTGTGCTTCCGGGAATTTGATGATACAGTGTCTGCATGG 1047  
Db 964 CAATGAACCTTTCCAGAGATGGAATGGTGTGCTTCCGGGAACATTTGACACAGTGTCTGCATGG 1023  
Qy 1048 CTGTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1107  
Db 1024 CTGTGCTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCTTGT 1083  
Qy 1108 CCTTGTAGTTACAGCAC-TTTCGGGTGGGAACCTTAAGGATACCTGCGAGTGAACAACTGGAG 1166  
Db 1084 CCTTGTAGTTACAGCACGTAATGTTGGGCACTCTAAGGAGACTGCGGTGACAAACCGGAG 1143  
Qy 1167 GAAGCGGGGAGCAGCTCAAGTCATCGGCCCTTTACGACAGGCTTACACAGTGTCTAC 1226  
Db 1144 GAAGTGGGAGTACGCTCAAGTCATCGGCCCTTTACGCCCTTGGCTTACACAGTGTCTAC 1203  
Qy 1227 AATGTAGTGTACAGAGGCGACTACACAGCGATGATGCGNATCTCAAAAGCCTATCG 1286  
Db 1204 AATGTGCGGTACAGAGGTTGCGAAGCGCGAGGTGGAGCTAATCCCAACAAACCGATCG 1263  
Qy 1287 TAGTCCAGATTGAGCTGTGCAACTCGACTCCATGAAGTAGGAAATCGTAGTAATCGCGGA 1346  
Db 1264 TAGTCCGAGTCCAGTCTTGCAACTCGACTGCTGAGTCCGNAATCGCTAGTAATCGCGAA 1323  
Qy 1347 TCAGAAATGCGCGGTGAATACGTTCCCGGGCCCTTGTACACACCGCCCTTACACCATGG 1406  
Db 1324 TCAGAAATGCGCGGTGAATACGTTCCCGGGCCCTTGTACACACCGCCCTTACACCATGG 1383  
Qy 1407 AGTTGATTGCAACCAAGTGTAGCTTAA-CTTAGTAGGCGGATCACACCGGTGTGGT 1465  
Db 1384 AGTGGGTTGCAACCAAGTGTAGCTTAACTTCCGGAGGACGCTTACCAACCGGTGTGAT 1443  
Qy 1466 CGATGACTGGGTGAAGTCGTAACCAAGTGTAGCGGTAGGGAACCTTCCGGCTGGATCAC 1523  
Db 1444 TCATGACTGGGTGAAGTCGTAACCAAGTGTAGCGGTAGGGAACCTTCCGGCTGGATCAC 1501

## RESULT 12

US-10-133-404A-1  
; Sequence 1, Application US/10133404A  
; Publication No. US20030104302A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsutomu Honma  
; APPLICANT: Tetsuya Yano  
; APPLICANT: Tsuyoshi No. US20030104302A1oto  
; APPLICANT: Shinya Kozaki  
; TITLE OF INVENTION: Construct and Method for Making It  
; FILE REFERENCE: CF016374  
; CURRENT APPLICATION NUMBER: US/10/133,404A  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: JP P2001-131694  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: JP P2001-208704  
; PRIOR FILING DATE: 2001-07-10  
; NUMBER OF SEQ ID NOS: 13  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain  
US-10-133-404A-1

Query Match

72.0%; Score 1098.6; DB 15; Length 1501;

Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
Qy 30 GCGCGAGGCTTAACACATGCAAGTCGAGCGGAACGATAGTAGCTTCTATTAGCGTC 89  
Db 9 GCGCGAGGCTTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTCTCTGAAATCA 66  
Qy 90 GAGNCGCGGACGGGTGAGTAATCTTAGGAATCTTACCTAGTAGTGGGGGATAGTCCGG 149  
Db 67 G---CGGCGAGCGGTGAGTAATGCTTAGGAATCTGCTTGTAGTGGGGGACAACTCTC 123  
Qy 150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCAATTAGACCTTG 208  
Db 124 GAAAGGAGCGCTAATACCGCATACGTCTCTACGGGAGAAAGCAGGGGACCTTCCGGCCCTTG 183  
Qy 209 CGCTATTAGATGAGCCTTAAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 268  
Db 184 CGCTATCAGATGAGCCTTAGGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 243  
Qy 269 ACATCTCTAGCTGTCTGAGAGGATGATCAGCCACACCGGACCTGACACACGCGCCGGA 328  
Db 244 ACATCTCTAGCTGTCTGAGAGGATGATCAGTCACACTGGAACCTGACACACGCTCCAGA 303  
Qy 329 CT-CTACGGGAGGAGCAGTGGGGAATATTGGAACAATGGNGGGAACCTCTGATCCAGCAT 387  
Db 304 CTCTACGGGAGGAGCAGTGGGGAATATTGGAACAATGGNGGGAACCTCTGATCCAGCAT 363  
Qy 388 GCGCGTGTGTGAAGAAGGCTTTTGGTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447  
Db 364 GCGCGTGTGTGAAGAAGGCTTTTGGTGTAAAGCACTTTAAGTGTGGAGGAAGGCAAT 423  
Qy 448 TCGGTTAATACCCGGGAGCAGTACATTCGATTCGAGAAATAGACACCGGCTTAACCTCTGTC 507  
Db 424 TAACTAATACCTTGTAGTGTGTTGAGTTTACCGACAGATAGACACCGGCTTAACCTCTGTC 483  
Qy 508 CAGCAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCGGGCGTAAAGCGA 567  
Db 484 CAGCAGCGCGGTAAATACAGAGGTTGCAAGCGTTAATCGGAATTAATCGGGCGTAAAGCGC 543  
Qy 568 GCGTAGTGGCTTCAATGATGAGTGAATCCCGGCTTAACTCGGAGTGAAGTGAAGTGAAGT 627  
Db 544 GCGTAGTGGCTTCAATGATGAGTGAATCCCGGCTTAACTCGGAGTGAAGTGAAGTGAAGT 603  
Qy 628 GAAACTGTAGCTAGTGTGAGGAGGAGTGAATTTTCAAGTGTAGCGGTGAAGTGAAGTGAAGT 687  
Db 604 AAACTGACAGCTAGTGTGAGGAGGAGTGAATTTTCAAGTGTAGCGGTGAAGTGAAGTGAAGT 663  
Qy 688 CGTAGAGATCTGAAGGAATACCGATGCGGAAGGAGGCTTCTGGCATCATACTGACACTG 747  
Db 664 CGTAGATATAGGAAGGAACACCGATGCGGAAGGAGGCTTCTGGCATCATACTGACACTG 723  
Qy 748 AGGCTCGAAGGAGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTAAACG 807  
Db 724 AGGTCGCAAGGAGTGGGTAGCAAAACAGGATTAGATACCTGGTAGTCCACCGCTAAACG 783  
Qy 808 ATGTCTACTAGTGTGGGTCCCTTGGAGCTTGTAGTACGAGCTTAAGTGAAGTGAAGTGAAGT 867  
Db 784 ATGTCAACTAGCTGTGGGAGCTTGTAGTGTGGGAGCTTAAGTGAAGTGAAGTGAAGTGAAGT 843  
Qy 868 CCGCTCGGAGTACCGCGCAAGGTTAAAACTCAAAATGAATGACGGGGCCCGCACAA 927  
Db 844 CCGCTCGGAGTACCGCGCAAGGTTAAAACTCAAAATGAATGACGGGGCCCGCACAA 903  
Qy 928 CCGTGGAGCATGTTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987  
Db 904 CCGTGGAGCATGTTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 963  
Qy 988 CACAGAACTTTGTAGATACAGAGTGCCTTCCGGAAATTTGTGATACAGGTGCTCATGG 1047  
Db 964 CAATGAACCTTTCCAGAGATGAGTGGTGCCTTCGGGAACATTTGACACAGTGTGCTCATGG 1023  
Qy 1048 CTGTGCTCAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCTTGT 1107

Db	1024	CTGTGTCGTCAGTCGTGTCGTCAGATGTTGGGTTAAAGTCCCTAATACGAGCGCAACCCCTTGT	1083
Qy	1108	CCTTAGTTACAGCAC--TTCCGGGTGGGAACCTCTAAGGATATCTGCCAGTGACAACTCGAG	1166
Db	1084	CCTTAGTTACAGCACGATTAATGGTGGGCATCTTAAGGAGATCTGCCGTGCACAAACCGGAG	1143
Qy	1167	GAAGCGGGGACGACGTCGAAGTCATCATGTCGCCCTTACGACACAGGGCTACACAGTGTCTAC	1226
Db	1144	GAAGGTGGGGATGACGTCGAAGTCATCATGTCGCCCTTTACGGCTGGGCTACACAGTGTCTAC	1203
Qy	1227	AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG	1286
Db	1204	AATGTCGGTACAGAGGGTTGCCNAGCGCGAGGTGGAGCTAATCCCAAAAACCGATCG	1263
Qy	1287	TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA	1346
Db	1264	TAGTCCGGATCGAGTCTGCAACTCGACTCGGTGAGTCGGATCGTAGTAATCGCGAA	1323
Qy	1347	TCAGAAATCCCGCGGTGAATACGTTTCCCGGGCCTTGTACACACCGCCCGTACACCATGGG	1406
Db	1324	TCAGAAATGTCGCGGTGAATACGTTTCCCGGGCCTTGTACACACCGCCCGTACACCATGGG	1383
Qy	1407	AGTTGATTGCAACCAAGATGTTAGCCCTAA-CTTAGTGAGGGCGAATCAACACGGTGTGGT	1465
Db	1384	AGTGGGTTGCACACAGAGTAGCTAGTCTAACTTCGGGAGGACGGTTACACGGGTGTGAT	1443
Qy	1466	CGATGACTGGGGTGAAGTCGTAAACAGGTTAGCCGTAGGGGAAACCTCGGGCTGGAATCAC	1523
Db	1444	TCATGACTGGGGTGAAGTCGTACCAAGTTAGCCGTAGGGGAACCTCGGGGTGATATCAC	1501

RESULT 13

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US-10-242-696-1
; Sequence 1, Application US/10242696
; Publication No. US20030180899A1
; GENERAL INFORMATION:
; APPLICANT: Honma, Tsutomu
; APPLICANT: Kobayashi, Toyoko
; APPLICANT: Yano, Tetsuya
; APPLICANT: Kobayashi, Shin
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Kenmoku, Takashi
; TITLE OF INVENTION: Process for producing polyhydroxyalkanoate by utilizing microorga
; FILE REFERENCE: 03500.015010.1
; CURRENT APPLICATION NUMBER: US/10/242,696
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: JP 11-371864
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371867
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371868
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 11-371869
; PRIOR FILING DATE: 12-27-1999
; PRIOR APPLICATION NUMBER: JP 2000-023024
; PRIOR FILING DATE: 01-31-2000
; PRIOR APPLICATION NUMBER: JP 2000-023025
; PRIOR FILING DATE: 01-31-2000
; PRIOR APPLICATION NUMBER: JP 2000-361323
; PRIOR FILING DATE: 11-28-2000
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; PERM P-17445
US-10-242-696-1

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Query Match 72.0%; Score 1098.6; DB 16; Length 1501;  
Best Local Similarity 85.9%; Pred. NO. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

Qy	30	GGCGGAGGCTTAAACATCATGCAATGCTAGCGGAAACGATGATAGTCTGCTATTAGCGGTC	89
Db	9	GGCGGAGGCTTAAACATCATGCAATGCTAGCGG--ATGACGGGAGCTTGTCTCTGAAATCA	66
Qy	90	GAGNGCCGACGGGTGAGTAAATCTTAGGAATCTACCTAGTAGTGGGGATAGCTCGGG	149
Db	67	G---CGCGGACGGGTGAGTAAATGCTTAGGAATCTGCTGGTAGTGGGGACAACTGCTC	123
Qy	150	GAACCTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCAATAGACCTTG	208
Db	124	GAAGGAGCGCTAATACCGCATACGCTTACGGGAGAAAGCAGGGACCTTCGGGCCCTTG	183
Qy	209	CGCTATTAGATGAGCCCTAAGTCGGATTAGCTAGATGCTGGGGTAAAGGCCCTACCATGGCG	268
Db	184	CGCTATCAGATGAGCCCTAGCTCGGATTAGCTAGTTGGTGAGGTAAATGGCTCACCAAGGCG	243
Qy	269	ACGATCTGTAGCTGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA	328
Db	244	ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA	303
Qy	329	CT-CTACGGGAGCAGCAGTGGGGAATATTGGACAATGNGGCAACCTCATCCAGCCAT	387
Db	304	CTCTACGGGAGGACAGTGGGGAATATTGGACAATGGCGGAAGGCTGATCAGCCAT	363
Qy	388	GC CGCGTGTGTGAAGAGGCTTTTGGTTGTAAAGCACATTTAAGCAGTGAAGAACTCT	447
Db	364	GCCCGTGTGTGAAGAGGCTTTCGGATTGTAAAGCACATTTAAAGTTGGGAGGAAGGCAT	423
Qy	448	TCGGTTAATACCCGGGACGATGACATTAGCTCAGAAATGAAGCACCGGCTAACTCTGTGC	507
Db	424	TAACTTAATACGTTAGTGTTTGACGCTTACCGACAGAATAAGCACCGGCTAACTCTGTGC	483
Qy	508	CAGCAGCCGGGTAAATACAGAGGCTCAAGCGTTAATCGGAAATCTTGGCGGTAAAGCGA	567
Db	484	CAGCAGCCGGGTAAATACAGAGGCTCAAGCGTTAATCGGAAATCTTGGCGGTAAAGCGC	543
Qy	568	CGGTAGTGTGCTTGATAAGTCAGATGTGAATCCCGGGCTTAACTTGGAACTGCATCT	627
Db	544	CGGTAGTGTGTTTGTAAAGTTGGAATGTGAAGACCCCGGCTCAACTGGGAACTGCAATC	603
Qy	628	GAACTGTTAGGCTAGATGAGTGAGAGGAAGTAGAAATTCAGGTGTAGCGGTGAATG	687
Db	604	AAAACTGACAAGCTAGATGTGTAGAGGGTGTGGAAATTTCTGTGTAGCGGTGAATG	663
Qy	688	CGTAGAGATCTGAAGGAATAACGATGCGAAGGACGCTTCTCGCATCATCTGACACTG	747
Db	664	CGTAGATATAGGAAGGAACACCAAGTGGGAAGCGGACCACTGGAATGATCTGACACTG	723
Qy	748	AGGCTCGAAAGCGTGGGTAGCAACACAGGATTAGATACCTGTAGTCCACCGCGTAAACG	807
Db	724	AGGTGCGAAGCGTGGGAGCAACAGGATTAGATACCTCGGTAGTCCACCGCGTAAACG	783
Qy	808	ATGTCTACTAGTCGTTGGGTCTCTTGAGGACTTAGTGAACGACGTAACGCAATAGTAGA	867
Db	784	ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAAACGATTAAAGTTGA	843
Qy	868	CCGCTCGGAGTACCGCCGCAAGGTTAAACTCAATGAATTAGCGGGGGCCGCGACAA	927
Db	844	CCGCTCGGAGTACCGCCGCAAGGTTAAACTCAATGAATTAGCGGGGGCCGCGACAA	903
Qy	928	CGCGTGAGCATGTGGTTTAATTCGATGCAACGCAAGAACTTACCTGCTCTTGACATA	987
Db	904	CGCGTGAGCATGTGGTTTAATTCGAGCAACGCAAGAACTTACAGGCTTGTGACATC	963
Qy	988	CACAGAACTTGTAGAGATACGAGAGTGCCTTCGGGAATGTGATACAGGTGCTGATGG	1047
Db	964	CAATGAACCTTCAGAGATGGATGGGTGCCTTCGGGAACAATTGAGACAGGTGCTGATGG	1023
Qy	1048	CTGTGCTGACGTCGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTGT	1107
Db	1024	CTGTGCTGACGTCGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTGT	1083
Qy	1108	CTTAGTTACAGCAC- TTCGGGTGGGAACCTCTAAGGATACCTCCAGTGACAACTGGAG	1166



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1084 CCTTAGTTACAGCAGTAAATGGTGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143
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1144 GAAGGTGGGGATGAGCTCAAGTCATCATGCGCCCTTACGCGCTTACACAGTCTTAC 1203
1227 AATGTAGGTACAGAGGGCAGCTACACAGCGATGTGATCGGAATCTCAAAAGCCATCG 1286
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; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms
; FILE REFERENCE: In The Same
; FILE REFERENCE: 03500.015001.1
; CURRENT APPLICATION NUMBER: US/10/411,319
; PRIORITY FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US 09/748,205
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

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Best Local Similarity 85.9%; Pred. No. 1.2e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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QY 209 CGCTATTAGATGAGCCTAAGTCGATAGTGTGGGGTAAAGGCTTACCATGCGC 268
DB 184 CGCTATCAGATGAGCCTAGGTCGATTAGCTAGTTGGTGAAGTAATGCTCACCAGGCG 243
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DB 484 CAGCAGCGCGGTAAATACAGAGGGTGAAGCGTTAATCGGAATTAATCTGGGCGTAAAGCGC 543
QY 568 GCGTAGTGGCTTGTAAAGTCAGATGTAAGTCCCGGGCTTAACCTGGGAACTGCACTCT 627
DB 544 GCGTAGTGGTGTGTTAAGTTGGATGTGAAGCCCGGGCTCAACCTGGGAACTGCACTTC 603
QY 628 GAAACTGTTAGCTAGAGTAGGTGAGAGGAGTAGAATTTTCAAGTGTAGCGGTGAATG 687
DB 604 AAACTGCAAGCTAGAGTAGGTGAGAGGTTGGAATTTTCTGTGTAGCGGTGAATG 663
QY 688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGAGCTTCTCTGGCATCATATCTGACACTG 747
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; Sequence 1, Application US/10649646  
; Publication No. US20040067576A1  
; GENERAL INFORMATION:  
; APPLICANT: Canon Inc.  
; TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms  
; TITLE OF INVENTION: In The Same  
; FILE REFERENCE: 03500.015001.2  
; CURRENT APPLICATION NUMBER: US/10/649,646  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR FILING DATE: 1999-12-27 JP 11-371863  
; PRIOR APPLICATION NUMBER: JP 2000-023078  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-023080  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-023083  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: JP 2000-095011  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-095012  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-095013  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: JP 2000-207089  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 2000-207091  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: JP 2000-359789  
; PRIOR FILING DATE: 2000-11-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1501  
; TYPE: DNA  
; ORGANISM: Pseudomonas jessenii 161 strain  
US-10-649-646-1  
Query Match 72.0%; Score 1098.6; DB 17; Length 1501;  
Best Local Similarity 85.9%; Pred. No. 1.2e-288;  
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;  
Qy 30 GCGCGCAGGCTTAACATGCAAGTCGAGCGGAACGATAGCTTGTCTATTAGGCGTC 89  
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Job time : 1140.89 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 05:59:04 ; Search time 234 Seconds  
(without alignments)  
480.663 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccggggacgatgacatta 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

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4: Geneseqn2001as.\*

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7: Geneseqn2002bs.\*

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9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	19	100.0	1526	AAC87531	AAC87531 Psychroba
C 3	16.4	86.3	86	ADM44619	Adm44619 Insect re
C 4	16.4	86.3	218	ADM44620	Adm44620 Insect re
C 5	16.4	86.3	584	AAC76269	AAC76269 Human ORF
C 6	16.4	86.3	1882	AAF21914	AAF21914 Human bre
C 7	16.4	86.3	1926	ABA06572	ABA06572 Human cDN
C 8	16.4	86.3	1926	ABV83909	ABV83909 Human pol
C 9	16.4	86.3	1987	AAZ52368	AAZ52368 NSEQ gene
C 10	16.4	86.3	1987	AAI42464	AAI42464 Human mat
C 11	16.4	86.3	1989	AA37044	AA37044 Human PRO
C 12	16.4	86.3	1989	AAF54255	AAF54255 DNA encod
C 13	16.4	86.3	1989	ACD68292	ACD68292 Novel hum
C 14	16.4	86.3	1989	ACH04394	ACH04394 Human cDN
C 15	16.4	86.3	1989	ACD67938	ACD67938 Novel hum
C 16	16.4	86.3	1989	ADC17945	ADC17945 Human PRO
C 17	16.4	86.3	1989	ADD70591	ADD70591 Human cDN
C 18	16.4	86.3	1989	ADD39668	ADD39668 Human cDN
C 19	16.4	86.3	1989	ADD70114	ADD70114 Human cDN
C 20	16.4	86.3	1989	ADD38235	ADD38235 Human cDN

C 21	16.4	86.3	1989	10	ADD39191	Add39191 Human	CDN
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C 23	16.4	86.3	1989	10	ADD40145	Add40145 Human	CDN
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C 25	16.4	86.3	1989	10	ADE19978	Ade19978 Human	CDN
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C 38	16.4	86.3	1989	12	ADH03441	Adh03441 Human	CDN
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C 40	16.4	86.3	1989	12	ADH61396	Adh61396 Human	CDN
C 41	16.4	86.3	1989	12	ADL94595	Adl94595 Human	CDN
C 42	16.4	86.3	1990	3	AAC58113	Aac58113 Human	PRO
C 43	16.4	86.3	2005	4	AAH13666	Aah13666 Human	CDN
C 44	16.4	86.3	2029	10	ADI21368	Adi21368 Novel hum	
C 45	16.4	86.3	2040	11	ACN89680	Acn89680 Breast ca	

ALIGNMENTS

RESULT 1

AAC87532/c

ID AAC87532 standard; DNA; 19 BP.

XX

AC AAC87532;

XX

DT 13-MAR-2001 (first entry)

XX

DE Psychrobacter pacificensis 16S rDNA probe, SEQ ID NO:2.

XX

KW 16S rDNA; species-specific detection; identification;

KW psychrophilic bacterium; oceanic circulation; Psychrobacter; probe; ss.

XX

OS Psychrobacter pacificensis.

XX

PN WO200071705-A1.

XX

PD 30-NOV-2000.

XX

PF 25-MAY-2000; 2000WO-JP003372.

XX

PR 25-MAY-1999; 95JP-00145342.

PR 30-MAR-2000; 2000WO-JP002045.

 XX | (AGEN ) AGENCY OF IND SCI & TECHNOLOGY. |

CC a novel method for detecting or specifically identifying Psychrobacter  
 CC pacificensis, Psychrobacter glacincola, and related species, or  
 CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence. The  
 CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
 CC species-specific detection of Psychrobacter pacificensis to study and  
 CC monitor its growth as an indicator of the circulation of deep-sea water.  
 CC The method of the invention is rapid, accurate and has high sensitivity,  
 CC and removes the need to separate and culture the biological materials.  
 CC The present sequence represents a specifically claimed Psychrobacter  
 CC pacificensis 16S rDNA oligonucleotide probe  
 XX  
 SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.3;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
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 Db 19 CCGGGGACGATGACATTA 1

## RESULT 2

AAC87531  
 ID AAC87531 standard; DNA; 1526 BP.

XX AC AAC87531;

XX DT 13-MAR-2001 (first entry)

XX DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.

XX KW 16S rDNA; species-specific detection; identification;  
 KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
 KW strain NIBH P2K6; ds.

XX OS Psychrobacter pacificensis.

XX PN W0200071705-A1.

XX PD 30-NOV-2000.

XX PF 25-MAY-2000; 2000WO-JP003372.

XX PR 25-MAY-1999; 99JP-00145342.

XX PR 30-MAR-2000; 2000WO-JP002045.

XX PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

XX PI Maruyama A, Kitamura K, Kurane R;

XX DR WPI; 2001-025158/03.

XX PT DNA probe originating from psychrotrophic bacterium applicable in species  
 PT -specific detection of the microorganism as indication in studying and  
 PT monitoring its growth and circulation of deep-sea water with sensitivity.

XX PS Claim 1; Page 30; 37pp; Japanese.

XX SQ The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
 CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
 CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
 CC for monitoring the growth of psychrophilic bacteria and the circulation  
 CC of deep-sea water. Psychrobacter pacificensis is an aerobic, Gram-  
 CC negative, non-motile, non-spore-forming oxidase-positive bacterium  
 CC originally isolated from the Japan Trench. The invention also relates to  
 CC a novel method for detecting or specifically identifying Psychrobacter  
 CC pacificensis, Psychrobacter glacincola, and related species, or  
 CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence. The  
 CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
 CC species-specific detection of Psychrobacter pacificensis to study and  
 CC monitor its growth as an indicator of the circulation of deep-sea water.  
 CC The method of the invention is rapid, accurate and has high sensitivity,

CC and removes the need to separate and culture the biological materials.  
 CC The present sequence represents the Psychrobacter pacificensis 16S rDNA  
 XX  
 SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 0 U; 3 Other;

Query Match 100.0%; Score 19; DB 4; Length 1526;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
 |||||  
 Db 458 CCGGGGACGATGACATTA 476

## RESULT 3

ADM44619

ID ADM44619 standard; DNA; 86 BP.

XX AC ADM44619;

XX DT 03-JUN-2004 (first entry)

XX DE Insect resistance associated N benthamiana DNA SeqID26.

XX KW Insect resistant phenotype; plant protectant; gene therapy;  
 KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
 KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX OS Nicotiana benthamiana.

XX PN W02003020025-A2.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027882.

XX PR 31-AUG-2001; 2001US-0316319P.

XX PA (DOWC ) DOW CHEM CO.

XX PI Shukla V, Meade T, Larrinua I;

XX DR WPI; 2003-290133/28.

XX PT New isolated nucleic acid having expression that results in an insect  
 PT resistant phenotype, useful for conferring insect resistance and for  
 PT producing insect-resistant plants.

XX PS Claim 1; SEQ ID NO 26; 396pp; English.

XX SQ This invention relates to a novel isolated nucleic acid comprising, or  
 CC hybridising under low stringent conditions to, any of the 1214 nucleic  
 CC acid sequences given in the specification, where the expression of the  
 CC nucleic acid in a plant results in an insect resistant phenotype. The  
 CC invention may be useful as a plant protectant or for gene therapy. The  
 CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
 CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
 CC useful for conferring insect resistance and for producing insect-  
 CC resistant plants. The present sequence is that of a DNA sequence of the  
 CC invention which may confer insect resistance to plants.

XX SQ Sequence 86 BP; 24 A; 16 C; 26 G; 20 T; 0 U; 0 Other;

Query Match 86.3%; Score 16.4; DB 11; Length 86;  
 Best Local Similarity 94.4%; Pred. No. 1.9e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGGGGACGATGACATTA 19  
 |||||  
 Db 11 CCGGGGACGATGACATTA 28

## RESULT 4

ADN44620  
ID ADM44620 standard; DNA; 218 BP.  
XX  
AC ADM44620;  
XX  
03-JUN-2004 (first entry)  
XX  
DE Insect resistance associated N benthamiana DNA SeqID27.  
XX  
XX insect resistant phenotype; plant protectant; gene therapy;  
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.  
XX  
OS Nicotiana benthamiana.  
XX  
PN WO2003020025-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-US027882.  
XX  
PR 31-AUG-2001; 2001US-0316319P.  
XX  
PA (DOWC) DOW CHEM CO.  
XX  
PI Shukla V, Meade T, Larrinua I;  
XX  
XX WPI; 2003-290133/28.  
XX  
PT New isolated nucleic acid having expression that results in an insect  
PT resistant phenotype, useful for conferring insect resistance and for  
PT producing insect-resistant plants.  
XX  
XX Claim 1; SEQ ID NO 27; 396pp; English.  
XX  
CC This invention relates to a novel isolated nucleic acid comprising, or  
CC hybridising under low stringent conditions to, any of the 1214 nucleic  
CC acid sequences given in the specification, where the expression of the  
CC nucleic acid in a plant results in an insect resistant phenotype. The  
CC invention may be useful as a plant protectant or for gene therapy. The  
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
CC useful for conferring insect resistance and for producing insect-  
CC resistant plants. The present sequence is that of a DNA sequence of the  
CC invention which may confer insect resistance to plants.  
XX  
SQ Sequence 218 BP; 60 A; 28 C; 45 G; 85 T; 0 U; 0 Other;  
  
Query Match 86.3%; Score 16.4; DB 11; Length 218;  
Best Local Similarity 94.4%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 CCGGGGACGATGACATTA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 11 CCGGGGACGATGACATTA 28  
  
RESULT 5  
AAC76269/c  
ID AAC76269 standard; cDNA; 584 BP.  
XX  
XX AAC76269;  
AC  
XX  
08-FEB-2001 (first entry)  
XX  
XX Human ORFX ORF1824 polynucleotide sequence SEQ ID NO:3647.  
DE  
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW

antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
neurodegenerative disorder; osteoarthritis; graft vs host disease;  
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
cholesterol ester storage; systemic lupus erythematosus; infection;  
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
bone damage; cartilage damage; antiinflammatory disease; coagulation;  
thrombosis; contraceptive; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200058473-A2.  
PN  
XX  
XX 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US008621.  
XX  
XX 31-MAR-1999; 99US-0127607P.  
PR  
XX 02-APR-1999; 99US-0127636P.  
PR  
XX 05-APR-1999; 99US-0127728P.  
PR  
XX 30-MAR-2000; 2000US-00540763.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
PI  
XX WPI; 2000-602362/57.  
DR  
XX P-PSDB; AAB42060.  
XX  
PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease.  
XX  
XX Claim 5; Page 2803; 5507pp; English.  
XX  
CC AACT7446 to AACT77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;  
CC antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;  
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;  
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The  
CC sequences can be used for determining the presence of or predisposition  
CC to, or preventing or treating pathological conditions associated with an  
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX  
CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
CC used to treat cancers, proliferative disorders, neurodegenerative  
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and  
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
XX  
SQ Sequence 584 BP; 74 A; 232 C; 183 G; 93 T; 0 U; 2 Other;  
  
Query Match 86.3%; Score 16.4; DB 3; Length 584;  
Best Local Similarity 94.4%; Pred. No. 2.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CCGGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 497 CTCGGGGACGATGACATT 480  
  
RESULT 6  
AAF21914/c  
ID AAF21914 standard; DNA; 1882 BP.  
XX  
XX AAF21914;  
AC  
XX

DT 27-MAR-2001 (first entry)

XX Human breast and ovarian cancer associated antigen gene SEQ ID 301.  
 DE Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 XX nontropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 KW antidiabetic; antiinflammatory; antitumor; vulnerary; anticonvulsant;  
 KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease; ds.  
 XX Homo sapiens.  
 OS  
 XX WO200055173-A1.  
 PN  
 XX 21-SEP-2000.  
 PD  
 XX 08-MAR-2000; 2000WO-US005881.  
 PF  
 XX 12-MAR-1999; 99US-0124270P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Ruben SM;  
 PI  
 XX WPI; 2000-611515/58.  
 DR  
 XX P-PSDB; AAB59011.  
 DR

XX New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention, treatment  
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and  
 PT neurological diseases.  
 XX  
 PS Claim 1; Page 712-713; 1299pp; English.  
 XX  
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nontropic;  
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;  
 CC antiinflammatory; antitumor; vulnerary; anticonvulsant; antibacterial;  
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and  
 CC protein sequences are used in the diagnosis of cancer, particularly  
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
 CC and agonists may also be used in the diagnosis, prevention and treatment  
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;  
 CC neurological diseases such as cerebral anoxia and epilepsy; and  
 CC infectious diseases  
 XX

SQ Sequence 1882 BP; 383 A; 616 C; 527 G; 350 T; 0 U; 6 Other;

Query Match 86.3%; Score 16.4; DB 3; Length 1882;

Best Local Similarity 94.4%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGGACGATGACATT 18

Db 546 CTCGGGGACGATGACATT 529

RESULT 7

ABA06572/c

ID ABA06572 standard; cDNA; 1926 BP.

XX

AC ABA06572;

XX 10-JAN-2002 (first entry)  
 DT  
 XX Human cDNA SEQ ID NO: 238.  
 DE  
 XX Human; gene therapy; neural disorder; immune system disorder;  
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
 KW pulmonary disorder; cardiovascular disorder; renal disorder;  
 KW proliferative disorder; inflammation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154474-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 17-JAN-2001; 2001WO-US001349.  
 PF  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR  
 XX 04-FEB-2000; 2000US-0180628P.  
 PR  
 XX 24-FEB-2000; 2000US-0184664P.  
 PR  
 XX 02-MAR-2000; 2000US-0186350P.  
 PR  
 XX 16-MAR-2000; 2000US-0189874P.  
 PR  
 XX 17-MAR-2000; 2000US-0190076P.  
 PR  
 XX 18-APR-2000; 2000US-0198123P.  
 PR  
 XX 19-MAY-2000; 2000US-0205515P.  
 PR  
 XX 07-JUN-2000; 2000US-0209467P.  
 PR  
 XX 28-JUN-2000; 2000US-0214866P.  
 PR  
 XX 30-JUN-2000; 2000US-0215135P.  
 PR  
 XX 07-JUL-2000; 2000US-0216647P.  
 PR  
 XX 07-JUL-2000; 2000US-0216880P.  
 PR  
 XX 11-JUL-2000; 2000US-0217487P.  
 PR  
 XX 11-JUL-2000; 2000US-0217496P.  
 PR  
 XX 14-JUL-2000; 2000US-0218290P.  
 PR  
 XX 26-JUL-2000; 2000US-0220963P.  
 PR  
 XX 26-JUL-2000; 2000US-0220964P.  
 PR  
 XX 14-AUG-2000; 2000US-0224518P.  
 PR  
 XX 14-AUG-2000; 2000US-0224519P.  
 PR  
 XX 14-AUG-2000; 2000US-0225213P.  
 PR  
 XX 14-AUG-2000; 2000US-0225214P.  
 PR  
 XX 14-AUG-2000; 2000US-0225266P.  
 PR  
 XX 14-AUG-2000; 2000US-0225267P.  
 PR  
 XX 14-AUG-2000; 2000US-0225268P.  
 PR  
 XX 14-AUG-2000; 2000US-0225270P.  
 PR  
 XX 14-AUG-2000; 2000US-0225447P.  
 PR  
 XX 14-AUG-2000; 2000US-0225757P.  
 PR  
 XX 14-AUG-2000; 2000US-0225758P.  
 PR  
 XX 14-AUG-2000; 2000US-0225759P.  
 PR  
 XX 18-AUG-2000; 2000US-0226279P.  
 PR  
 XX 22-AUG-2000; 2000US-0226681P.  
 PR  
 XX 22-AUG-2000; 2000US-0226686P.  
 PR  
 XX 22-AUG-2000; 2000US-0227182P.  
 PR  
 XX 23-AUG-2000; 2000US-0227009P.  
 PR  
 XX 30-AUG-2000; 2000US-0228924P.  
 PR  
 XX 01-SEP-2000; 2000US-0229287P.  
 PR  
 XX 01-SEP-2000; 2000US-0229343P.  
 PR  
 XX 01-SEP-2000; 2000US-0229344P.  
 PR  
 XX 01-SEP-2000; 2000US-0229345P.  
 PR  
 XX 03-SEP-2000; 2000US-0229509P.  
 PR  
 XX 05-SEP-2000; 2000US-0229513P.  
 PR  
 XX 06-SEP-2000; 2000US-0230437P.  
 PR  
 XX 06-SEP-2000; 2000US-0230438P.  
 PR  
 XX 08-SEP-2000; 2000US-0231242P.  
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 XX 08-SEP-2000; 2000US-0231243P.  
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 XX 08-SEP-2000; 2000US-0231244P.  
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 XX 08-SEP-2000; 2000US-0231413P.  
 PR  
 XX 08-SEP-2000; 2000US-0231414P.  
 PR  
 XX 08-SEP-2000; 2000US-0232080P.  
 PR  
 XX 12-SEP-2000; 2000US-0232081P.  
 PR  
 XX 14-SEP-2000; 2000US-0232397P.  
 PR  
 XX 14-SEP-2000; 2000US-0232398P.  
 PR  
 XX 14-SEP-2000; 2000US-0232399P.



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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0234584P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244674P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.

PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251899P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-476161/51.
DR P-PSDB; ABB10350.
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition.
XX Claim 1; SEQ ID NO 238; 859pp + Sequence Listing; English.
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a cDNA of the invention
XX
SQ Sequence 1926 BP; 395 A; 654 C; 536 G; 341 T; 0 U; 0 Other;
Query Match 86.3%; Score 16.4; DB 4; Length 1926;
Best Local Similarity 94.4%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGACATT 18
| | | | | | | | | | | | | | | | | |
Db 590 CTCGGGACGATGACATT 573

RESULT 8
ABV83909/c
ID ABV83909 standard; cDNA; 1926 BP.
XX
AC ABV83909;
XX
DT 09-DEC-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 238.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antischlicking; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
XX gene; ss.
XX Homo sapiens.
XX
PN US2002090672-A1.
XX
PD 11-JUL-2002.
XX
PF 17-JAN-2001; 2001US-00764853.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214896P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
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PT New mammalian DNA sequences encoding transmembrane, receptor or secreted  
PT PRO polypeptides, useful for screening of potential peptide or small  
XX molecule inhibitors of the relevant receptor/ligand interactions.  
XX Claim 2; Fig 45; 773pp; English.  
XX  
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
CC transmembrane and receptor PRO proteins can be used for screening of  
CC potential peptide or small molecule inhibitors of the relevant  
CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
CC encoding then have various industrial applications, including uses as  
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR  
CC primers and hybridisation probes used in the isolation of the PRO  
CC polypeptides from the present invention  
XX  
SQ Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 U; 0 Other;  
Query Match 86.3%; Score 16.4; DB 3; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCCGGGACGATGACATT 18  
Db 732 CTCGGGACGATGACATT 715  
RESULT 12  
AAF54255/c  
ID AAF54255 standard; DNA; 1989 BP.  
XX  
AC AAF54255;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE DNA encoding protein of the invention #23.  
XX  
KW Secreted; transmembrane; gene therapy; ss.  
XX  
OS Unidentified.  
XX  
PN WO200078961-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 18-FEB-2000; 2000WO-US004342.  
XX  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US02011.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2001-071395/08.  
XX  
XX Secreted and transmembrane proteins and nucleic acids designated PRO,  
PT useful as hybridization probes, in chromosome and gene mapping and gene  
PT therapy.  
XX  
PS Claim 2; Fig 45; 787pp; English.  
XX

PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
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PR 18-NOV-1998; 98US-0108904P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
PI WPI; 2000-237871/20.  
DR P-PSDB; AAY99362.  
XX

CC The present invention relates to secreted and transmembrane proteins.  
CC These proteins and the DNA encoding them may be used as hybridization  
CC probes, in chromosome and gene mapping and in the generation of anti-  
CC sense RNA and DNA. They may also be used to generate either  
CC transgenic animals or knockout animals which are in turn useful for  
CC development and screening of therapeutically useful reagents. The nucleic  
CC acids may also be used in gene therapy

SQ Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 U; 0 Other;

Query Match 86.3%; Score 16.4; DB 4; Length 1989;

Best Local Similarity 94.4%; Pred. No. 2.5e-02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCGGGACGATGACATT 18

Db 732 CTCGGGACGATGACATT 715

#### RESULT 13

ACD68292/c

ID ACD68292 standard; cDNA; 1989 BP.

XX AC ACD68292;

XX AC ACD68292;

XX DT 17-SEP-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO1293 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; angiogenesis;

XX KW endothelial cell proliferation; wound healing; immune response;

XX KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;

XX KW cardiac insufficiency disorder; calcium flux; inflammation;

XX KW vascular endothelial growth factor-stimulated proliferation;

XX KW mammalian kidney mesangial cell proliferation; Berger disease;

XX KW nephropathy; Schlemmer-Henoch purpura; celiac disease; Crohn's disease;

XX KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;

XX KW pancreatic beta-cell precursor cell differentiation; thalassemias;

XX KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;

XX KW cartilage disorder; sports injury; arthritis; gene; ss.

XX KW Homo sapiens.

OS Homo sapiens.

XX US2003073130-A1.

XX 17-APR-2003.

XX 11-DEC-2001; 2001US-00015869.

XX 01-SEP-1998; 98US-0098716P.

XX 01-SEP-1998; 98US-0098723P.

XX 01-SEP-1998; 98US-0098749P.

XX 01-SEP-1998; 98US-0098750P.

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XX 02-SEP-1998; 98US-0098821P.

XX 02-SEP-1998; 98US-0098843P.

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XX 10-SEP-1998; 98US-0099754P.

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XX 10-SEP-1998; 98US-0099815P.

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(GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
PI Williams PM, Wood WI;  
XX WPI; 2003-492259/46.

DR P-PSDB; ABO44457.  
XX

PI Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries and  
PT arthritis.

Query Match 86.3%; Score 16.4; DB 9; Length 1989;

Best Local Similarity 94.4%; Pred. No. 2.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
Db 732 CTCGGGGACGATGACATT 715

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ID ACD67938/c  
XX ACD67938 standard; cDNA; 1989 BP.  
XX AC ACD67938;  
XX DT 17-SEP-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1293 cDNA.  
XX KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;  
XX KW tissue typing; chromosome identification; vaccine; gene; ss.  
XX OS Homo sapiens.  
XX PN US2003073129-A1.  
XX PD 17-APR-2003.  
XX PF 04-SEP-2001; 2001US-00946374.  
XX PR 01-SEP-1998; 98US-0098716P.  
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PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.



Search completed: April 12, 2005, 09:07:38  
Job time : 241 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 08:44:34 ; Search time 88 Seconds  
(without alignments)  
353.287 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19  
Sequence: 1 cccggggacgatgacatta 19

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/ECTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.4	85.3	2132	3	US-09-552-322-1
C 2	15.4	81.1	601	4	US-09-949-016-136302
C 3	15.4	81.1	2338	4	US-09-582-337-1
C 4	15.4	81.1	2350	3	US-09-187-478-1
C 5	15.4	81.1	2350	3	US-09-292-036-1
C 6	15.4	81.1	51049	4	US-09-949-016-15571
C 7	15	78.9	636	4	US-09-902-540-8517
C 8	15	78.9	6855	4	US-09-902-540-897
C 9	14.8	77.9	99	1	US-08-427-097-12
C 10	14.8	77.9	99	2	US-08-878-957-12
C 11	14.8	77.9	170	1	US-08-419-078-5
C 12	14.8	77.9	170	1	US-08-419-078-6
C 13	14.8	77.9	170	1	US-08-726-883-5
C 14	14.8	77.9	170	1	US-08-726-883-6
C 15	14.8	77.9	300	1	US-08-419-078-4
C 16	14.8	77.9	300	1	US-08-726-883-4
C 17	14.8	77.9	384	4	US-09-389-681-451
C 18	14.8	77.9	384	4	US-09-620-405B-451
C 19	14.8	77.9	384	4	US-09-433-826B-451
C 20	14.8	77.9	384	4	US-09-604-287A-451
C 21	14.8	77.9	384	4	US-09-834-759-451
C 22	14.8	77.9	384	4	US-09-590-751A-451
C 23	14.8	77.9	384	4	US-09-551-621-451
C 24	14.8	77.9	879	4	US-09-248-796A-7856
C 25	14.8	77.9	1322	1	US-08-419-078-1
C 26	14.8	77.9	1322	1	US-08-726-883-1
C 27	14.8	77.9	1323	4	US-09-023-655-55

28	14.8	77.9	1594	4	US-09-270-767-14907	Sequence 14907, A
C 29	14.8	77.9	1752	1	US-08-427-097-13	Sequence 13, Appl
C 30	14.8	77.9	1752	1	US-08-427-097-19	Sequence 19, Appl
C 31	14.8	77.9	1752	2	US-08-878-957-13	Sequence 13, Appl
C 32	14.8	77.9	1752	2	US-08-878-957-19	Sequence 19, Appl
C 33	14.8	77.9	2936	4	US-09-976-594-1044	Sequence 1044, Ap
C 34	14.8	77.9	28843	4	US-09-949-016-17325	Sequence 17325, A
C 35	14.8	77.9	134987	4	US-09-949-016-15348	Sequence 15348, A
C 36	14.8	77.9	134987	4	US-09-949-016-15349	Sequence 15349, A
C 37	14.8	77.9	134987	4	US-09-949-016-15350	Sequence 15350, A
C 38	14.8	77.9	134987	4	US-09-949-016-15507	Sequence 15507, A
C 39	14.8	77.9	134987	4	US-09-949-016-15508	Sequence 15508, A
C 40	14.8	77.9	134987	4	US-09-949-016-15509	Sequence 15509, A
C 41	14.8	77.9	203475	4	US-09-949-016-14516	Sequence 14516, A
C 42	14.8	77.9	203475	4	US-09-949-016-14517	Sequence 14517, A
C 43	14.8	77.9	203475	4	US-09-949-016-14518	Sequence 14518, A
C 44	14.8	77.9	203475	4	US-09-949-016-14519	Sequence 14519, A
C 45	14.8	77.9	203475	4	US-09-949-016-17226	Sequence 17226, A

#### ALIGNMENTS

##### RESULT 1

US-09-552-322-1/c  
; Sequence 1, Application US/09552322  
; Patent No. 6436642  
; GENERAL INFORMATION:  
; APPLICANT: Gould-Rothberg  
; APPLICANT: Rastelli  
; TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING  
; FILE REFERENCE: 15966-548  
; CURRENT APPLICATION NUMBER: US/09/552,322  
; CURRENT FILING DATE: 2000-04-19  
; PRIOR FILING DATE: 1999-04-20  
; PRIOR APPLICATION NUMBER: 60/193,203  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2132  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-552-322-1

Query Match 86.3%; Score 16.4; DB 3; Length 2132;  
Best Local Similarity 94.4%; Pred. No. 78;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCCGGGACGATGACATT 18

Db 861 CTCGGGACGATGACATT 844

##### RESULT 2

US-09-949-016-136302/c  
; Sequence 136302 Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136302
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136302

Query Match      81.1%; Score 15.4; DB 4; Length 601;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACAT 17
   ||||| ||||| |||||
Db 77 CCCGGGGACATGACAT 61

RESULT 3
US-09-582-337-1
; Sequence 1, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582.337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(212)
; NAME/KEY: CDS
; LOCATION: (213)..(1256)
; NAME/KEY: 3'UTR
; LOCATION: (1257)..(2338)
; NAME/KEY: polyA_signal
; LOCATION: (2297)..(2302)
US-09-582-337-1

Query Match      81.1%; Score 15.4; DB 4; Length 2338;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACAT 17
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Db 1194 CCCGGGGACATGACAT 1210

RESULT 4
US-09-187-478-1
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; APPLICANT: Allen, Margaret L.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use
; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187,478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350

; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match      81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACAT 17
   ||||| ||||| |||||
Db 1193 CCCGGGGACATGACAT 1209

RESULT 5
US-09-292-036-1
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDORUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIBROI100-1
; CURRENT APPLICATION NUMBER: US/09/292.036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-292-036-1

Query Match      81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACAT 17
   ||||| ||||| |||||
Db 1193 CCCGGGGACATGACAT 1209

RESULT 6
US-09-949-016-15571
; Sequence 15571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 15571  
LENGTH: 51049  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15571

Query Match 81.1%; Score 15.4; DB 4; Length 51049;  
Best Local Similarity 94.1%; Pred. No. 3.3e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGACAT 17  
|||||  
DB 13209 CCCGGGACGATGACAT 13225

## RESULT 7

US-09-902-540-8517  
Sequence 8517, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 8517  
LENGTH: 636  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-8517

Query Match 78.9%; Score 15; DB 4; Length 636;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGAC 15  
|||||  
DB 265 CCCGGGACGATGAC 279

## RESULT 8

US-09-902-540-897  
Sequence 897, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 897  
LENGTH: 6855  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-897

Query Match 78.9%; Score 15; DB 4; Length 6855;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGAC 15

DB 4043 CCCGGGACGATGAC 4057  
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## RESULT 9

US-08-427-097-12/c  
Sequence 12, Application US/08427097  
Patent No. 5668294  
GENERAL INFORMATION:  
APPLICANT: Meagher, Richard B.  
APPLICANT: Sommers, Anne O.  
TITLE OF INVENTION: Metal Resistance Sequences and  
TITLE OF INVENTION: Transgenic Plants  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/427,097  
FILING DATE: 21-APR-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 40-94  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 99 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotide"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-427-097-12

Query Match 77.9%; Score 14.8; DB 1; Length 99;  
Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCGGGACGATGACATTA 19  
|||||  
DB 96 CCCGGGTCGATGACATA 79

## RESULT 10

US-08-878-957-12/c  
Sequence 12, Application US/08878957  
Patent No. 5965796  
GENERAL INFORMATION:  
APPLICANT: Meagher, Richard B.  
APPLICANT: Sommers, Anne O.  
APPLICANT: Rugh, Clayton L.  
TITLE OF INVENTION: Metal Resistance Sequences and  
TITLE OF INVENTION: Transgenic Plants  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder

```
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/878,957
  FILING DATE: 19-JUN-1997
  CLASSIFICATION: 800
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/427,097
    FILING DATE: 21-APR-1995
  ATTORNEY/AGENT INFORMATION:
    NAME: Ferber, Donna M.
    REGISTRATION NUMBER: 33,878
    REFERENCE/DOCKET NUMBER: 40-94A
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (303) 499-8080
    TELEFAX: (303) 499-8089
    TELEX:
  INFORMATION FOR SEQ ID NO: 12:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 99 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: other nucleic acid
    DESCRIPTION: /desc = "Oligonucleotide"
    HYPOTHETICAL: NO
    ANTI-SENSE: NO
    US-08-878-957-12

Query Match          77.9%; Score 14.8; DB 2; Length 99;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGGGGACGATGACATTA 19
Db 96 CCGGGGTCGATGACAA 79

RESULT 11
US-08-419-078-5
Sequence 5, Application US/08419078
Patent No. 5587306
GENERAL INFORMATION:
  APPLICANT: HAWKINS, PHILLIP R.
  APPLICANT: SEILHAMER, JEFFREY J.
  TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
  NUMBER OF SEQUENCES: 13
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  STREET: 3330 HILLVIEW AVENUE
  CITY: PALO ALTO
  STATE: CA
  COUNTRY: USA
  ZIP: 94304
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: Patent In Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/419,078
    FILING DATE:
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: LUTHER, BARBARA J.
    REGISTRATION NUMBER: 33954
    REFERENCE/DOCKET NUMBER: PF0030 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-855-0555
    TELEFAX: 415-855-0572
  INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 170 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      IMMEDIATE SOURCE:
      LIBRARY: Fibroblast
      CLONE: 054216
    US-08-419-078-6

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-855-0555
  TELEFAX: 415-855-0572
  INFORMATION FOR SEQ ID NO: 5:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 170 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      IMMEDIATE SOURCE:
      LIBRARY: Corneal Stroma
      CLONE: 046611
    US-08-419-078-5

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
Db 117 CCGGTCGAGGATGACATT 134

RESULT 12
US-08-419-078-6
Sequence 6, Application US/08419078
Patent No. 5587306
GENERAL INFORMATION:
  APPLICANT: HAWKINS, PHILLIP R.
  APPLICANT: SEILHAMER, JEFFREY J.
  TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
  NUMBER OF SEQUENCES: 13
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  STREET: 3330 HILLVIEW AVENUE
  CITY: PALO ALTO
  STATE: CA
  COUNTRY: USA
  ZIP: 94304
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: Patent In Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/419,078
    FILING DATE:
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: LUTHER, BARBARA J.
    REGISTRATION NUMBER: 33954
    REFERENCE/DOCKET NUMBER: PF0030 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415-855-0555
    TELEFAX: 415-855-0572
  INFORMATION FOR SEQ ID NO: 6:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 170 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      IMMEDIATE SOURCE:
      LIBRARY: Fibroblast
      CLONE: 054216
    US-08-419-078-6

Query Match          77.9%; Score 14.8; DB 1; Length 170;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
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Db 117 CCCGTGGAGGATGACATT 134  
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## RESULT 13

US-08-726-883-5  
; Sequence 5, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Corneal Stroma  
; CLONE: 046611  
US-08-726-883-5

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
||||| ||| ||| ||| ||| ||| |||  
Db 117 CCCGTGGAGGATGACATT 134

## RESULT 14

US-08-726-883-6  
; Sequence 6, Application US/08726883  
; Patent No. 5676946  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO

; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,883  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/419,078  
; FILING DATE: 10-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-855-0572  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Fibroblast  
; CLONE: 054216  
US-08-726-883-6

Query Match 77.9%; Score 14.8; DB 1; Length 170;  
Best Local Similarity 88.9%; Pred. No. 4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCGGGGACGATGACATT 18  
||||| ||| ||| ||| ||| ||| |||  
Db 117 CCCGTGGAGGATGACATT 134

## RESULT 15

US-08-419-078-4  
; Sequence 4, Application US/08419078  
; Patent No. 5587306  
; GENERAL INFORMATION:  
; APPLICANT: HAWKINS, PHILLIP R.  
; APPLICANT: SEILHAMER, JEFFREY J.  
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,078  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33954  
; REFERENCE/DOCKET NUMBER: PF0030 US  
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; LIBRARY: Hybrid T/B Lymphoblast
; CLONE: 043866
;
US-08-419-078-4

Query Match      77.9%; Score 14.8; DB 1; Length 300;
Best Local Similarity 88.9%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCGGGGACGATGACATT 18
Db      239 CCGGTGGAGGATGACATT 256
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Search completed: April 12, 2005, 10:01:56  
Job time : 90 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 09:31:24 ; Search time 289 Seconds  
(without alignments)  
398.409 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccgggacgatgacatta 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*\*

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- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.4	86.3	1329	17	US-10-169-395-18
C 2	16.4	86.3	1882	9	US-09-925-298-301
C 3	16.4	86.3	1882	14	US-10-102-806-301
C 4	16.4	86.3	1926	9	US-09-764-853-238
C 5	16.4	86.3	1987	9	US-09-818-143-20
C 6	16.4	86.3	1989	10	US-09-946-374-76
C 7	16.4	86.3	1989	14	US-10-006-856A-76
C 8	16.4	86.3	1989	14	US-10-006-818A-76
C 9	16.4	86.3	1989	14	US-10-006-485A-76
C 10	16.4	86.3	1989	14	US-10-013-907A-76
C 11	16.4	86.3	1989	14	US-10-015-499A-76

C 12	16.4	86.3	1989	14	US-10-015-393A-76	Sequence 76, Appl
C 13	16.4	86.3	1989	14	US-10-015-869A-76	Sequence 76, Appl
C 14	16.4	86.3	1989	14	US-10-012-121A-76	Sequence 76, Appl
C 15	16.4	86.3	1989	14	US-10-006-116A-76	Sequence 76, Appl
C 16	16.4	86.3	1989	14	US-10-006-117A-76	Sequence 76, Appl
C 17	16.4	86.3	1989	14	US-10-017-527A-76	Sequence 76, Appl
C 18	16.4	86.3	1989	14	US-10-013-913A-76	Sequence 76, Appl
C 19	16.4	86.3	1989	14	US-10-007-194A-76	Sequence 76, Appl
C 20	16.4	86.3	1989	14	US-10-013-430A-76	Sequence 76, Appl
C 21	16.4	86.3	1989	14	US-10-011-671A-76	Sequence 76, Appl
C 22	16.4	86.3	1989	14	US-10-012-755A-76	Sequence 76, Appl
C 23	16.4	86.3	1989	14	US-10-015-386A-76	Sequence 76, Appl
C 24	16.4	86.3	1989	15	US-10-011-692A-76	Sequence 76, Appl
C 25	16.4	86.3	1989	15	US-10-006-768A-76	Sequence 76, Appl
C 26	16.4	86.3	1989	15	US-10-017-610A-76	Sequence 76, Appl
C 27	16.4	86.3	1989	15	US-10-006-063A-76	Sequence 76, Appl
C 28	16.4	86.3	1989	15	US-10-020-063A-76	Sequence 76, Appl
C 29	16.4	86.3	1989	15	US-10-015-391A-76	Sequence 76, Appl
C 30	16.4	86.3	1989	15	US-10-017-407A-76	Sequence 76, Appl
C 31	16.4	86.3	1989	15	US-10-011-833A-76	Sequence 76, Appl
C 32	16.4	86.3	1989	15	US-10-006-041A-76	Sequence 76, Appl
C 33	16.4	86.3	1989	15	US-10-015-822A-76	Sequence 76, Appl
C 34	16.4	86.3	1989	15	US-10-015-387A-76	Sequence 76, Appl
C 35	16.4	86.3	1989	15	US-10-006-130A-76	Sequence 76, Appl
C 36	16.4	86.3	1989	16	US-10-006-172A-76	Sequence 76, Appl
C 37	16.4	86.3	1989	16	US-10-017-253A-76	Sequence 76, Appl
C 38	16.4	86.3	1989	16	US-10-015-392A-76	Sequence 76, Appl
C 39	16.4	86.3	1989	16	US-10-017-306A-76	Sequence 76, Appl
C 40	16.4	86.3	1989	16	US-10-017-867A-76	Sequence 76, Appl
C 41	16.4	86.3	1989	16	US-10-012-064A-76	Sequence 76, Appl
C 42	16.4	86.3	1989	16	US-10-013-909A-76	Sequence 76, Appl
C 43	16.4	86.3	1989	16	US-10-015-671A-76	Sequence 76, Appl
C 44	16.4	86.3	1989	16	US-10-015-610A-76	Sequence 76, Appl
C 45	16.4	86.3	1989	16	US-10-012-137A-76	Sequence 76, Appl

#### ALIGNMENTS

RESULT 1  
US-10-169-395-18/c  
; Sequence 18, Application US/10169395  
; Publication No. US20040034192A1  
; GENERAL INFORMATION:  
; APPLICANT: KATO, Seishi  
; APPLICANT: KIMURA, Tomoko  
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING  
; TITLE OF INVENTION: THESE PROTEINS  
; FILE REFERENCE: 01997.015100.US  
; CURRENT APPLICATION NUMBER: US/10/169,395  
; CURRENT FILING DATE: 2002-11-29  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-585  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-588  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: JP 2000-2299  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-26862  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: JP 2000-58367  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: PCT/JP00/09359  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 150  
; SEQ ID NO 18  
; LENGTH: 1329  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-169-395-18

Query Match 86.3%; Score 16.4; DB 17; Length 1329;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 999 CTCGGGACGATGACATT 982

## RESULT 2

US-09-925-298-301/c  
; Sequence 301, Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103  
; CURRENT APPLICATION NUMBER: US/09/925,298  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 301  
; LENGTH: 1882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (22)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (223)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1840)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1843)  
; OTHER INFORMATION: n equals a,t,g, or c  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-298-301

Query Match 86.3%; Score 16.4; DB 9; Length 1882;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18  
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Db 546 CTCGGGACGATGACATT 529

## RESULT 3

US-10-102-806-301/c  
; Sequence 301, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; CURRENT FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 301  
; LENGTH: 1882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (22)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (223)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1840)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1849)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-102-806-301

Query Match 86.3%; Score 16.4; DB 14; Length 1882;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 546 CTCGGGACGATGACATT 529

## RESULT 4

US-09-764-853-238/c  
; Sequence 238, Application US/09764853  
; Patent No. US20020090672A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PJZ06  
; CURRENT APPLICATION NUMBER: US/09/764,853  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 939  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 238  
; LENGTH: 1926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-853-238

Query Match 86.3%; Score 16.4; DB 9; Length 1926;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 590 CTCGGGACGATGACATT 573

## RESULT 5

US-09-818-143-20/c  
; Sequence 20, Application US/09818143  
; Patent No. US20020019000A1  
; GENERAL INFORMATION:  
; APPLICANT: Walker, Michael G.  
; APPLICANT: Volkmut, Wayne  
; APPLICANT: Klingler, Tod M.  
; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES  
; FILE REFERENCE: PB-0004 CIP  
; CURRENT APPLICATION NUMBER: US/09/818,143  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PERL Program  
; SEQ ID NO 20  
; LENGTH: 1987  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: 3948614CB1  
US-09-818-143-20

Query Match 86.3%; Score 16.4; DB 9; Length 1987;  
Best Local Similarity 94.4%; Pred. No. 1.4e-02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18  
DB 733 CTCGGGACGATGACATT 716

## RESULT 6

US-09-946-374-76/c  
; Sequence 76, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808

; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
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; PRIOR FILING DATE: 1998-09-16  
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; PRIOR FILING DATE: 1998-09-17  
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; PRIOR FILING DATE: 1998-09-17  
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; PRIOR FILING DATE: 1998-09-17  
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; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
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; PRIOR FILING DATE: 1998-09-18  
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; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
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; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
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; PRIOR APPLICATION NUMBER: 60/101915  
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; PRIOR FILING DATE: 1998-09-24  
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; PRIOR FILING DATE: 1998-09-29



US-10-006-818A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e-02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGGACGATGACATT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 732 CTCGGGACGATGACATT 715

## RESULT 9

US-10-006-485A-76/c  
; Sequence 76, Application US/10006485A  
; Publication No. US20030064062A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC9  
; CURRENT APPLICATION NUMBER: US/10/006,485A  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 60/098716  
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; PRIOR APPLICATION NUMBER: 60/098843  
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;; PRIOR APPLICATION NUMBER: 60/106023  
;; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCCGGGACGATGACATT 18

Db 732 CTCGGGACGATGACATT 715  
RESULT 10  
US-10-013-907A-76/c  
; Sequence 76, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-907A-76

Query Match 86.3%; Score 16.4; DB 14; Length 1989;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCCGGGACGATGACATT 18  
Db 732 CTCGGGACGATGACATT 715

RESULT 11  
US-10-015-499A-76/c  
; Sequence 76, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PIC42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 76  
; LENGTH: 1989

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18
   |||||
Db 732 CTCGGGGACGATGACATT 715

RESULT 12
US-10-015-393A-76/c
; Sequence 76, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18
   |||||
Db 732 CTCGGGGACGATGACATT 715

RESULT 13
US-10-015-869A-76/c
; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
```

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18
   |||||
Db 732 CTCGGGGACGATGACATT 715

RESULT 14
US-10-012-121A-76/c
; Sequence 76, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-121A-76

Query Match      86.3%; Score 16.4; DB 14; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18
   |||||
Db 732 CTCGGGGACGATGACATT 715

RESULT 15
US-10-006-116A-76/c
; Sequence 76, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
```

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C15  
CURRENT APPLICATION NUMBER: US/10/006.116A  
CURRENT FILING DATE: 2001-12-16  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
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PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
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PRIOR FILING DATE: 1998-10-01  
PRIOR APPLICATION NUMBER: 60/102965  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: 60/103258  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103314  
PRIOR FILING DATE: 1998-10-07



; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 14; Length 1989;

Best Local Similarity 94.4%; Pred. No. 1.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATT 18

Db 732 CTCGGGACGATGACATT 715

Search completed: April 12, 2005, 10:50:17  
Job time : 290 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 08:13:54 ; Search time 1738 Seconds  
(without alignments)  
416.123 Million cell updates/sec

Title: US-09-979-558a-1\_COPY\_458\_476

Perfect score: 19

Sequence: 1 cccgggacgatgacatta 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	91.6	695	9 AG416365	AG416365 Mus muscu
C 2	17.4	91.6	793	9 CR004289	CR004289 Forward s
C 3	16.4	86.3	337	7 W92952	W92952 zd92e10.r1
C 4	16.4	86.3	340	1 AA037563	AA037563 zk34a03.r
C 5	16.4	86.3	369	7 W45082	W45082 zc21g10.r1
C 6	16.4	86.3	419	7 CN395703	CN395703 170004240
C 7	16.4	86.3	443	7 CN918724	CN918724 030207ABP
C 8	16.4	86.3	513	1 AA115144	AA115144 z110f09.r
C 9	16.4	86.3	531	7 CO610497	CO610497 DG8-94n3
C 10	16.4	86.3	533	1 A1817726	A1817726 wk25e07.x
C 11	16.4	86.3	537	7 W16559	W16559 zb11b12.r1
C 12	16.4	86.3	539	1 A1772402	A1772402 EST253502
C 13	16.4	86.3	554	4 B1627185	B1627185 RH68421.5
C 14	16.4	86.3	562	2 AW963853	AW963853 EST375926
C 15	16.4	86.3	594	7 CO598991	CO598991 DG8-174n1
C 16	16.4	86.3	595	2 BF342569	BF342569 602013893
C 17	16.4	86.3	682	4 BG127540	BG127540 EST473282
C 18	16.4	86.3	768	4 B1758715	B1758715 603024016
C 19	16.4	86.3	799	4 B1754114	B1754114 603027673
C 20	16.4	86.3	817	7 CO596974	CO596974 DG8-138n1
C 21	16.4	86.3	903	5 BQ881886	BQ881886 AGENCOURT
C 22	16.4	86.3	957	5 BQ177752	BQ177752 AGENCOURT
C 23	16.4	86.3	1008	5 BX439049	BX439049 BX439049
C 24	16.4	86.3	1054	1 AL553402	AL553402 AL553402

C 25	16.4	86.3	1060	5 BUI34659	BUI34659 603121881
C 26	16.4	86.3	1129	5 BM924224	BM924224 AGENCOURT
C 27	16.4	86.3	1650	3 CF592046	CF592046 full1-leng
C 28	16.4	86.3	1987	2 AW888223	AW888223 MXRA8 Hum
C 29	16	84.2	373	6 CA269132	CA269132 SCRURT306
C 30	16	84.2	435	1 A1329817	A1329817 b8f06ne.r
C 31	16	84.2	511	1 A1397616	A1397616 NCSC5C8T7
C 32	16	84.2	517	2 AW186852	AW186852 BNLGH1597
C 33	16	84.2	639	1 AV849197	AV849197 AV849197
C 34	16	84.2	648	1 A1398536	A1398536 NCM07A9T7
C 35	16	84.2	686	1 AV849138	AV849138 AV849138
C 36	16	84.2	701	8 BH954585	BH954585 odi78c12.
C 37	16	84.2	709	8 BH954543	BH954543 odi78b12.
C 38	16	84.2	831	8 BH423226	BH423226 BOHSZ48TR
C 39	16	84.2	3342	9 CL982185	CL982185 OeIFSC046
C 40	15.8	83.2	192	8 BZ672389	BZ672389 PUBN32TD
C 41	15.8	83.2	215	1 AV025145	AV025145 AV025145
C 42	15.8	83.2	237	5 BP105595	BP105595 BP105595
C 43	15.8	83.2	243	4 BM106925	BM106925 511009 MA
C 44	15.8	83.2	269	7 CF613570	CF613570 CES008156
C 45	15.8	83.2	289	5 BQ640964	BQ640964 SSH-Bbb1c

#### ALIGNMENTS

RESULT 1	AG416365	695 bp	DNA	linear	GSS 03-JUN-2004
LOCUS	Mus musculus molossinus DNA, clone:MSMg01-278N11.T7, genomic survey				
DEFINITION	sequence.				
ACCESSION	AG416365				
VERSION	AG416365.1	GI:48059339			
KEYWORDS	GSS.				
SOURCE	Mus musculus molossinus				
ORGANISM	Mus musculus molossinus				
REFERENCE	1				
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.				
TITLE	BAC end Sequences of Library MSMg01				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 695)				
AUTHORS	Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gscc.riken.jp, URL: http://hgp.gscc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)				
COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : T7 LIBRARY Vector : pBACE3.6 R.Site 1 : EcoRI. R.Site 2 : EcoRI. Location/Qualifiers 1. .695 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMg01-278N11.T7" /sex="male" /tissue_type="mixture of kidney and spleen" /clone_lib="MSMg01 Mouse Male BAC Library"				

## ORIGIN

Query Match 91.6%; Score 17.4; DB 9; Length 695;  
 Best Local Similarity 94.7%; Pred. No. 3.le+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
 |||||  
 Db 568 CCGGGGACGATGATCA 550

## RESULT 2

CR004289/c  
 LOCUS 793 bp DNA linear GSS 05-JUL-2004  
 DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and  
 chromosome engineering clone MHPN182j15, genomic survey sequence.

ACCESSION CR004289

VERSION 1 GI:49737280

KEYWORDS GSS; genome survey sequence; MICER.

SOURCE Mus musculus (house mouse)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 793)

REFERENCE  
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.

TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER

## FEATURES

source  
 1..793  
 /organism="Mus musculus"  
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 /clone\_lib="MHPN182j15"  
 /clone\_lib="MHPN"

## ORIGIN

Query Match 91.6%; Score 17.4; DB 9; Length 793;  
 Best Local Similarity 94.7%; Pred. No. 3.le+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATTA 19  
 |||||  
 Db 270 CCGGGGACGATGATCA 252

## RESULT 3

W92952  
 LOCUS 337 bp mRNA linear EST 25-NOV-1996  
 DEFINITION z929e10.r1 Soares\_fetal\_heart\_NBHH19W Homo sapiens cDNA clone  
 IMAGE:356970 5', similar to contains element MER22 repetitive  
 element ;, mRNA sequence.

ACCESSION W92952

VERSION 1 GI:1422104

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS Hillier,B., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and  
 Wilson,R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800

Pax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 998 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence stop: 279.

## FEATURES

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 1..337  
 /organism="Homo sapiens"  
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 /db\_xref="GDB:1273514"  
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 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal heart NBHH19W"  
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCATCTTTTTCCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NBHL19W."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 7; Length 337;  
 Best Local Similarity 94.4%; Pred. No. 1e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGGGACGATGACATT 18  
 |||||  
 Db 256 CTCGGGACGATGACATT 273

## RESULT 4

AA037563  
 LOCUS 340 bp mRNA linear EST 10-MAY-1997  
 DEFINITION zK34a03.r1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone  
 IMAGE:484684 5', mRNA sequence.

ACCESSION AA037563

VERSION AA037563.1 GI:1512663

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
 Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,  
 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,  
 Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,  
 Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,  
 Trevasakis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.  
 and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags  
 Genome Res. 6 (9), 807-828 (1996)

JOURNAL 97044478

MEDLINE 8889549

## COMMENT

Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.



```

CN918724      CN918724      443 bp      mRNA      linear      EST 07-JUN-2004
LOCUS         030207ABPB006067HT (ABPB) M9 root tips Malus x domestica cDNA clone
DEFINITION    ABPB006067, mRNA sequence.
ACCESSION     CN918724
VERSION       CN918724.1 GI:48391537
KEYWORDS      EST.
SOURCE        Malus x domestica (cultivated apple)
ORGANISM      Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 443)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES      Location/Qualifiers
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             /mol_type="mRNA"
             /db_xref="taxon:3750"
             /clone="ABPB006067"
             /tissue_type="Root tips (distal 1.5 cm)"
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             /note="vector: pluescript SK(-); Library sequenced by
             Genesis Research & Development"
ORIGIN
Query Match      86.3%; Score 16.4; DB 7; Length 443;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 392 CCGGGGACGATGACTT 409

RESULT 8
AA115144
LOCUS         z110f09.t1 Soares_pregnant uterus_NBHPU Homo sapiens cDNA clone
DEFINITION    IMAGE:501545 5', mRNA sequence.
ACCESSION     AA115144
VERSION       AA115144.1 GI:1670568
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 513)
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

CN918724      CN918724      443 bp      mRNA      linear      EST 07-JUN-2004
LOCUS         030207ABPB006067HT (ABPB) M9 root tips Malus x domestica cDNA clone
DEFINITION    ABPB006067, mRNA sequence.
ACCESSION     CN918724
VERSION       CN918724.1 GI:48391537
KEYWORDS      EST.
SOURCE        Malus x domestica (cultivated apple)
ORGANISM      Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 443)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES      Location/Qualifiers
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             /clone_lib="(ABPB) M9 root tips"
             /note="vector: pluescript SK(-); Library sequenced by
             Genesis Research & Development"
ORIGIN
Query Match      86.3%; Score 16.4; DB 7; Length 443;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 392 CCGGGGACGATGACTT 409

RESULT 8
AA115144
LOCUS         z110f09.t1 Soares_pregnant uterus_NBHPU Homo sapiens cDNA clone
DEFINITION    IMAGE:501545 5', mRNA sequence.
ACCESSION     AA115144
VERSION       AA115144.1 GI:1670568
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 513)
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

```

```

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 392.
Location/Qualifiers
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             /db_xref="taxon:9606"
             /clone="IMAGE:501545"
             /sex="female"
             /dev_stage="adult"
             /lab_host="DH10B"
             /clone_lib="Soares_pregnant uterus_NBHPU"
             /note="Organ: uterus; Vector: pTV73-Pac; Site 1: Not I;
             Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
             oligo(dT) primer [5',
             AACTGGAAGATTCCGGCGCGCTTTTCTTTT 3'],
             double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Not I and cloned into the Not I
             and Eco RI sites of the modified pTV73 vector. Library
             went through one round of normalization. Library
             constructed by M. Fatima Bonaldo."
ORIGIN
Query Match      86.3%; Score 16.4; DB 1; Length 513;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 18 CTCGGGACGATGACATT 35

RESULT 9
CO610497/c
LOCUS         DG8-94n3 DG8-testis Canis familiaris cDNA 3', mRNA sequence.
DEFINITION    CO610497
ACCESSION     CO610497
VERSION       CO610497.1 GI:50456061
KEYWORDS      EST.
SOURCE        Canis familiaris (dog)
ORGANISM      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 531)
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loebbert, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
             1..531
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             /mol_type="mRNA"
             /strain="Beagle"
             /db_xref="taxon:9615"
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Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCGGGGACGATGACATTA 19

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Db      407 CCGGGGACGTTGACATTA 390
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RESULT 10
A1817726
LOCUS
DEFINITION
  A1817726 533 bp mRNA linear EST 21-DEC-1999
  mRNA sequence.
ACCESSION
  A1817726
VERSION
  A1817726.1 GI:5436805
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 533)
REFERENCE
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
  Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
  Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
  Wilson, R.
  The WashU-Merck EST Project
  Unpublished (1995)
JOURNAL
  Contact: Wilton RK
  Washington University School of Medicine
  444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Seq primer: ETPprimer
  High quality sequence stop: 342.
  Location/Qualifiers
    1..537
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    /mol_type="mRNA"
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    /db_xref="taxon:9606"
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    /clone_lib="Soares fetal lung NbHL19W"
    /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
    modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
    strand cDNA was primed with a Not I - oligo(dT) primer
    [5'-TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTT-3'],
    double-stranded cDNA was size selected, ligated to Eco RI
    adaptors (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT7T3 vector
    (Pharmacia). Library went through one round of
    normalization to a Cot = 5. Library constructed by Bento
    Soares and M.Fatima Bonaldo. This library was constructed
    from the same fetus as the fetal heart library, Soares
    fetal heart NbHL19W."
FEATURES
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    /clone_lib="Soares fetal lung NbHL19W"
    /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
    modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
    strand cDNA was primed with a Not I - oligo(dT) primer
    [5'-TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTT-3'],
    double-stranded cDNA was size selected, ligated to Eco RI
    adaptors (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT7T3 vector
    (Pharmacia). Library went through one round of
    normalization to a Cot = 5. Library constructed by Bento
    Soares and M.Fatima Bonaldo. This library was constructed
    from the same fetus as the fetal heart library, Soares
    fetal heart NbHL19W."
ORIGIN
  Query Match 86.3%; Score 16.4; DB 1; Length 533;
  Best Local Similarity 94.4%; Pred. No. 1e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
  |||||
Db 35 CTCGGGGACGATGACATT 18

RESULT 12
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LOCUS
DEFINITION
  A1772402 539 bp mRNA linear EST 18-MAY-2001
  EST253502 tomato resistant, Cornell Lycopersicon esculentum CDNA
  clone CLER2H9, mRNA sequence.
ACCESSION
  A1772402
VERSION
  A1772402.1 GI:5270443
KEYWORDS
  EST.
SOURCE
  Lycopersicon esculentum (tomato)
ORGANISM
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
  1 (bases 1 to 539)
REFERENCE
  D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
  Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,
  Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksey, S.D.,
  Soares, M., and M.Fatima Bonaldo.
  This library was constructed from the same fetus as the fetal heart library, Soares
  fetal heart NbHL19W."
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    /lab_host="DH10B (ampicillin resistant)"
    /clone_lib="Soares fetal lung NbHL19W"
    /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
    modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
    strand cDNA was primed with a Not I - oligo(dT) primer
    [5'-TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTT-3'],
    double-stranded cDNA was size selected, ligated to Eco RI
    adaptors (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified pT7T3 vector
    (Pharmacia). Library went through one round of
    normalization to a Cot = 5. Library constructed by Bento
    Soares and M.Fatima Bonaldo. This library was constructed
    from the same fetus as the fetal heart library, Soares
    fetal heart NbHL19W."
ORIGIN
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  Best Local Similarity 94.4%; Pred. No. 1e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
  |||||
Db 503 CTCGGGGACGATGACATT 520

RESULT 11
W16559/c
LOCUS
DEFINITION
  W16559 537 bp mRNA linear EST 29-APR-1996
  zb1b12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone
  IMAGE:301727 5' similar to contains element MS1 repetitive element
  ;, mRNA sequence.
ACCESSION
  W16559
VERSION
  W16559.1 GI:1290941
  
```

```

Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
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                /dev_stage="4-week old"
                /lab_host="SOLR"
                /clone_lib="Tomato resistant, Cornell"
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                XhoI; cLER - Tomato Pseudomonas Resistant EST Library.
                Directionally cloned cDNAs inserted into pBluescript
                SK(-) at 5' end with EcoRI and 3' end with XhoI site."
ORIGIN
Query Match      86.3%; Score 16.4; DB 1; Length 539;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 455 CCGGGGACGATGACTT 438

RESULT 13
Bi627185
LOCUS      554 bp mRNA linear EST 07-SEP-2001
DEFINITION Drosophila melanogaster normalized Head pF1c-1
            Drosophila melanogaster cDNA clone RH68421 5 similar to igl:
            FBan018285 GO: (ligand binding or carrier (GO:0005488); calmodulin
            binding (GO:0005516)) located on: 2R 51E5-51E7;: 08/24/2001, mRNA
            sequence.
ACCESSION  Bi627185
VERSION    Bi627185.1 GI:15522710
KEYWORDS  EST.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 554)
            Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B.,
            Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
            George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
            Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
            Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
            Rubin,G.M.
            BDGP/HMI RH Drosophila EST Project
            Unpublished (2001)
            Contact: Stapleton, M.
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: RH.684 row: B column: 9
            High quality sequence stop: 462.
            Location/Qualifiers
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/clone="RH68421"
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/lab_host="DH5-alpha Tona"
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pF1c-1"
/note="Organ: head; Vector: pF1c1; Site 1: XhoI; Site 2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
ORIGIN
Query Match      86.3%; Score 16.4; DB 4; Length 554;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 456 CCGGGGACGATGACATT 473

RESULT 14
AW963853/c
LOCUS      562 bp mRNA linear EST 01-JUN-2000
DEFINITION EST375926 MAGE resequenes, MAGH Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW963853
VERSION    AW963853.1 GI:8153689
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 562)
            Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
            Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
            Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 194
            Seq primer: Reverse.
            Location/Qualifiers
                1..562
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /note="Vector: pBluescriptSKm"
ORIGIN
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Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGGGGACGATGACATT 18
    |||||
Db 62 CTCGGGACGATGACATT 45

RESULT 15
CO598991/c
LOCUS      594 bp mRNA linear EST 21-JUL-2004
DEFINITION DG8-374n16 DG8-testis Canis familiaris cDNA 3', mRNA sequence.
ACCESSION  CO598991
VERSION    CO598991.1 GI:50444555
KEYWORDS  EST.
SOURCE     Canis familiaris (dog)

```



ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 594)  
AUTHORS Schluter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,  
Henrich, J. and Loebbert, R.  
TITLE Dog arrayTAG cDNA clone collection  
JOURNAL Unpublished (2004)  
COMMENT Contact: Thomas Schluter  
LION bioscience AG  
Walhoferstrasse 98, D-69123 Heidelberg, Germany  
Tel: +49 6221 4038 150  
Fax: +49 6221 4038 290  
Email: Thomas.Schluter@lionbioscience.com.

FEATURES  
source  
1..594  
    /organism="Canis familiaris"  
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Best Local Similarity 94.4%; Pred. No. 1e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 2 CCGGGGACGATGACATTA 19  
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Db 407 CCGGGGACGTTGACATTA 390

Search completed: April 12, 2005, 10:00:26  
Job time : 1746 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:02:04 ; Search time 6689 Seconds  
(without alignments)  
11054.367 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
Sequence: 1 ttgatcatggtccagatt.....acctgcggtggtacacctc 1526

Scoring table: OMAIGO-NUC<sub>2</sub>  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_to.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1526	100.0	1526	1	AB016057	AB016057 Psychroba
2	1526	100.0	1526	6	E58427	E58427 DNA probe f
3	1124	73.7	1520	1	AB016059	AB016059 Psychroba
4	1098	72.0	1473	1	PSP551093	AJ551093 Psychroba
5	1091	71.5	1473	1	PSP551098	AJ551098 Psychroba
6	1047	68.6	1473	1	PSP551101	AJ551101 Psychroba
7	1004	65.8	1403	1	AB094456	AB094456 Psychroba
8	971	63.6	1531	1	AB016055	AB016055 Psychroba
9	953	62.5	995	1	AF194191	AF194191 Unculture
10	856	56.1	1530	1	AB016058	AB016058 Psychroba
11	655	42.9	1684	1	PSP551107	AJ551107 Psychroba
12	646	42.3	1536	1	AB016054	AB016054 Psychroba
13	566	37.1	1425	1	AF505739	AF505739 Bacterium
14	566	37.1	1441	1	AF165598	AF165598 Unculture
15	566	37.1	1445	1	AF468383	AF468383 Arctic se
16	566	37.1	1449	1	AF165583	AF165583 Unculture
17	566	37.1	1459	1	AY167310	AY167310 Psychroba
18	566	37.1	1463	1	AY167301	AY167301 Psychroba
19	566	37.1	1476	1	AF505743	AF505743 Bacterium

20	566	37.1	1483	1	AF468396	AF468396 Arctic se
21	566	37.1	1485	1	AY167308	AY167308 Psychroba
22	566	37.1	1493	1	AF505746	AF505746 Gamma pro
23	566	37.1	1498	1	PGL313425	AJ313425 Psychroba
24	553	36.2	1462	1	AB094458	AB094458 Psychroba
25	531	34.8	717	1	PSP244768	AJ244768 Psychroba
26	526	34.5	529	1	AF194193	AF194193 Unculture
27	523	34.3	1496	1	AY057116	AY057116 Psychroba
28	515	33.7	1462	1	PGU85879	U85879 Psychrobact
29	515	33.7	1539	1	AY573041	AY573041 Psychroba
30	508	33.3	704	1	PSF244770	AJ244770 Psychroba
31	485	31.8	700	1	PSF244767	AJ244767 Psychroba
32	485	31.8	705	1	PSF244771	AJ244771 Psychroba
33	484	31.7	1454	1	AY167289	AY167289 Psychroba
34	473	31.0	1478	1	AF517755	AF517755 Psychroba
35	472	30.9	1475	1	AY443042	AY443042 Psychroba
36	471	30.9	1494	1	PSF244766	AJ244766 Psychroba
37	462	30.3	810	1	AY220707	AY220707 Unculture
38	446	29.2	1493	1	AF505725	AF505725 Bacterium
39	445	29.2	1463	1	AY167281	AY167281 Psychroba
40	435	28.5	1426	1	PSP272303	AJ272303 Psychroba
41	423	27.7	1494	1	AY722804	AY722804 Psychroba
42	416	27.3	1489	1	AY167286	AY167286 Psychroba
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45	404	26.5	1507	1	AY738757	AY738757 Psychroba

ALIGNMENTS

AB016057 1526 bp DNA linear BCT 10-MAY-2000  
Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,  
strain:NIBH P2K6(T) (=IFO 16279(T)).

ACCESSION AB016057.1 GI:6691638

VERSION AB016057

KEYWORDS 16S ribosomal RNA.

SOURCE Psychrobacter pacificensis

ORGANISM Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Moraxellaceae; Psychrobacter.

REFERENCE 1 (sites)

Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.

Phylogenetic analysis of psychrophilic bacteria isolated from the

Japan Trench, including a description of the deep-sea species

Psychrobacter pacificensis sp. nov

Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)

JOURNAL MEDLINE 20222194

PUBMED 10758895

REFERENCE 2 (bases 1 to 1526)

Maruyama,A. and Kitamura,K.

Direct Submission

TITLE Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of

Bioscience and Human-Technology, Department of Applied and

Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,

Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,

Fax:+81-298-54-8412)

FEATURES Location/Qualifiers

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ORIGIN

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Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GAAACGATGATAGCTTCTATTAGGCGTTCGAGCNGCCGGACGGGTGAGTAATCTTAGGA 120
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Db 721 CAGCTTCTGGCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAG 780
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Db 781 ATACCTTGGTAGTCCAGCGGTAAACGATGCTACTAGTCTGTGGTCCCTTGGAGACTT 840
Qy 841 AGTGACGAGCTAACGCAATAGTAGACCGCTCGGAGTACCGCCGCAAGGTTAAACT 900
Db 841 AGTGACGAGCTAACGCAATAGTAGACCGCTCGGAGTACCGCCGCAAGGTTAAACT 900
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DEFINITION DNA probe for detecting novel psychrophile.  
ACCESSION E58427

VERSION B58427.1 GI:18622289

KEYWORDS JP 2000333680-A/1.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1526)

AUTHORS Maruyama, A., Kitamura, K. and Kurane, R.

TITLE DNA probe for detecting novel psychrophile

JOURNAL Patent: JP 2000333680-A 1 05-DEC-2000;

COMMENT AGENCY OF IND SCIENCE & TECHNOL

OS Psychrobacter pacificus

PN JP 2000333680-A/1

PD 05-DEC-2000

PF 25-MAY-1999 JP 1999145342

PR AKIHIKO MARUYAMA, KEIKO KITAMURA, RYUICHIRO KURANE PC

C12N15/09, C12N1/20, C12Q1/68// (C12N15/09, C12R1:01), (C12N1/20, PC

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PC C12N15/00, (C12N15/00, C12R1:01)

CC Key

FT irna Location/Qualifiers

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RESULT 3  
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DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence, strain:NIBH P2K18.

ACCESSION AB016059

VERSION AB016059.1 GI:6691640

KEYWORDS 16S ribosomal RNA.

SOURCE Psychrobacter pacificensis

ORGANISM Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE 1 (sites)  
 Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T. Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov. Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000) 20222194

JOURNAL PUBMED 10758895

REFERENCE 2 (bases 1 to 1520)  
 Maruyama, A. and Kitamura, K. Direct Submission Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail: maruyama@nibh.go.jp, Tel: +81-298-54-6062, Fax: +81-298-54-6412)

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RESULT 4  
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LOCUS Psychrobacter sp. wp8 partial 16S rRNA gene, isolate wp8. 17-MAY-2004  
DEFINITION Psychrobacter sp. wp8 partial 16S rRNA gene, isolate wp8.  
ACCESSION AJ551093  
VERSION AJ551093.1 GI:34525808  
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
SOURCE Psychrobacter sp. wp8  
ORGANISM Psychrobacter sp. wp8  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE  
1 Wang, F., Wang, P., Chen, M. and Xiao, X.  
Isolation of extremophiles with the detection and retrieval of  
Shewanella strains in deep-sea sediments from the west Pacific  
Extremophiles 8 (2), 165-168 (2004)  
JOURNAL  
PUBMED 15064982  
REFERENCE  
2 (bases 1 to 1473)  
Xiao, X.  
Direct Submission  
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic  
Resources, Third Institute of Oceanography, SOA, Daxuelu 178,  
Xiamen, 361005, CHINA

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TITLE Isolation of extremophiles with the detection and retrieval of Shewanella strains in deep-sea sediments from the west Pacific

JOURNAL Extremophiles 8 (2), 165-168 (2004)

PUBMED 15064982

REFERENCE 2 (bases 1 to 1473)

AUTHORS Xiao,X.

TITLE Direct Submission

JOURNAL Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic Resources, Third Institute of Oceanography, SOA, Daxuelu 178, Xiamen, 361005, CHINA

FEATURES

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## RESULT 6

LOCUS P5P51101 1473 bp DNA linear BCT 17-MAY-2004  
 DEFINITION Psychrobacter sp. wp21 partial 16S rRNA gene, isolate wp21.  
 ACCESSION AJ551101  
 VERSION AJ551101.1 GI:34525815  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
 SOURCE Psychrobacter sp. wp21  
 ORGANISM Psychrobacter sp. wp21  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.  
 REFERENCE 1  
 AUTHORS Wang, F., Wang, P., Chen, M. and Xiao, X.  
 TITLE Isolation of extremophiles with the detection and retrieval of Shewanella strains in deep-sea sediments from the west Pacific  
 JOURNAL Extremophiles 8 (2), 165-168 (2004)  
 PUBMED 15064982  
 REFERENCE 2 (bases 1 to 1473)  
 AUTHORS Xiao, X.  
 TITLE Direct Submission  
 JOURNAL Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic Resources, Third Institute of Oceanography, SOA, Daxuelu 178, Xiamen, 361005, CHINA  
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RESULT 7
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LOCUS Psychrobacter sp. MJYP.15.12 gene for 16S rRNA, partial sequence.
ACCESSION AB094456
VERSION AB094456.1 GI:27807566
KEYWORDS
SOURCE Psychrobacter sp. MJYP.15.12
ORGANISM Psychrobacter; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.

REFERENCE
AUTHORS Inagaki, F., Suzuki, M., Takai, K., Oida, H., Sakamoto, T., Aoki, K.,
Nealson, K. H. and Horikoshi, K.
TITLE Microbial Communities Associated with Geological Horizons in
Coastal Subseafloor Sediments from the Sea of Okhotsk
JOURNAL Appl. Environ. Microbiol. 69 (12), 7224-7235 (2003)
PUBMED 14660370
REFERENCE 2 (bases 1 to 1403)
AUTHORS Inagaki, F.
DIRECT SUBMISSION
SUBMITTED (23-OCT-2002) Fumio Inagaki, Japan Marine Science &
Technology Center, Subground Animalcule Retrieval (SUGAR) Project,
Frontier Research System for Extremophiles; Natsushima-cho 2-15,
Yokosuka 237-0061, Japan (E-mail: inagaki@jamstec.go.jp,
Tel: 81-468-67-9687, Fax: 81-468-67-9715)
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TITLE Phylogenetic analysis of psychrophilic bacteria isolated from the Japan Trench, including a description of the deep-sea species Psychrobacter pacificensis sp. nov.  
JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt-2, 835-846 (2000)  
MEDLINE 20222194  
PUBMED 10758895  
REFERENCE 2 (bases 1 to 1531)  
AUTHORS Maruyama, A. and Kitamura, K.  
TITLE Direct Submission  
JOURNAL Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of Bioscience and Human-Technology, Department of Applied and Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566, Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062, Fax:+81-298-54-6412)

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SOURCE uncultured Psychrobacter a2  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter; environmental samples.  
REFERENCE 1 (bases 1 to 995)  
AUTHORS Todorov, J.R., Chistoserdov, A.Y. and Aller, J.Y.  
TITLE Molecular analysis of microbial communities in mobile deltaic muds of Southeastern Papua New Guinea  
JOURNAL FEMS Microbiol. Ecol. 33 (2), 147-155 (2000)  
PUBMED 10967214  
REFERENCE 2 (bases 1 to 995)  
AUTHORS Todorov, J.R., Aller, J.Y. and Chistoserdov, A.Y.  
TITLE Direct Submission  
JOURNAL Submitted (13-OCT-1999) Marine Sciences Research Center, State University of New York at Stony Brook, Stony Brook, NY 11794-5000, USA  
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DEFINITION Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
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ACCESSION  AB016058
VERSION    AB016058.1  GI:6691639
KEYWORDS   16S ribosomal RNA.
SOURCE     Psychrobacter pacificensis
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
            Moraxellaceae; Psychrobacter.
REFERENCE  1 (sites)
AUTHORS    Maruyama,A., Honda,D., Yamamoto,H., Kitamura,K. and Higashihara,T.
TITLE       Phylogenetic analysis of psychrophilic bacteria isolated from the
            Japan Trench, including a description of the deep-sea species
            Psychrobacter pacificensis sp. nov
JOURNAL     Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
MEDLINE    20222194
PUBMED     10758895
REFERENCE  2 (bases 1 to 1530)
AUTHORS    Maruyama,A. and Kitamura,K.
TITLE       Direct Submission
JOURNAL     Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
            Bioscience and Human-Technology, Department of Applied and
            Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
            Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
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Qy 1268 AATCTCAAAAGCCTATCTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGTAAGTAGG 1327
Db 1268 AATCTCAAAAGCCTATCTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGTAAGTAGG 1327
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Db 1328 AATCGCTAGTAATCCGCGATCAGAAATCCGCGGTGAATACGTTCCCGGGCCCTTGACACA 1387
Qy 1388 CCGCCGCTCACACATGGGAGTTGATTGCAACGAGTGGTTAGCTTAAGTAGGAGG 1447
Db 1388 CCGCCGCTCACACATGGGAGTTGATTGCAACGAGTGGTTAGCTTAAGTAGGAGG 1447
Qy 1448 CGATCACACGCTGTGT 1465
Db 1448 CGATCACACGCTGTGT 1465
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```
RESULT 11
PSP51107 PSP51107 1684 bp DNA linear BCT 17-MAY-2004
LOCUS Psychrobacter sp. wp30 partial 16S rRNA gene, isolate wp30.
DEFINITION
ACCESSION AJ551107
VERSION AJ551107.1 GI:34525821
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Psychrobacter sp. wp30
ORGANISM Psychrobacter sp. wp30
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Psychrobacter.
REFERENCE
1 Wang, F., Wang, P., Chen, M. and Xiao, X.
AUTHORS
TITLE Isolation of extremophiles with the detection and retrieval of
JOURNAL Shewanella strains in deep-sea sediments from the west Pacific
PUBLISHED Extremophiles 8 (2), 165-168 (2004)
REFERENCE 15064982
2 (bases 1 to 1684)
AUTHORS Xiao, X.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
Xiamen, 361005, CHINA
FEATURES
Location/Qualifiers
source 1. .1684
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gene
rRNA
ORIGIN
Query Match 42.9%; Score 655; DB 1; Length 1684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 368 GGGAAACCCCTGATCCAGCATGCGCGTGTGTAAGAAGGCGCTTTTGGTTGTAAAGCACTT 427
Db 383 GGGAAACCCCTGATCCAGCATGCGCGTGTGTAAGAAGGCGCTTTTGGTTGTAAAGCACTT 442
Qy 428 TAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTAGCTGCAGAATA 487
Db 443 TAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGACGATGACATTAGCTGCAGAATA 502
Qy 488 AGCACGGCTAACTCTGTGCGCAGCAGCGCGTAAATACAGAGGGTGCAGCGTTAATCGG 547
Db 503 AGCACGGCTAACTCTGTGCGCAGCAGCGCGTAAATACAGAGGGTGCAGCGTTAATCGG 562
Qy 548 AATTACTGGCGCTAAAGCGAGCGTAGTGGCTTGATAAGTCAGATGTGAATCCCGGGGC 607
Db 563 AATTACTGGCGCTAAAGCGAGCGTAGTGGCTTGATAAGTCAGATGTGAATCCCGGGGC 622
Qy 608 TTAACTTGGGAACTGCATCTGAAACTGTGTTAGGCTAGAGTAGGTGAGAGGAAGTAGAATT 667
Db 623 TTAACTTGGGAACTGCATCTGAAACTGTGTTAGGCTAGAGTAGGTGAGAGGAAGTAGAATT 682
Qy 668 TCAGGTGTAGCGGTGAATCGGTAGAGATCTGAAGGAATACCGATGCGAAGGCGAGCTTC 727
Db 683 TCAGGTGTAGCGGTGAATCGGTAGAGATCTGAAGGAATACCGATGCGAAGGCGAGCTTC 742
Qy 728 CTGGCATCATACTACACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCT 787
Db 743 CTGGCATCATACTACACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCT 802
Qy 788 GGTAGTCCACGCGTAAACGATGTCTACTAGTGTGGGTCCCTTGAGGACTTAGTGACG 847
Db 803 GGTAGTCCACGCGTAAACGATGTCTACTAGTGTGGGTCCCTTGAGGACTTAGTGACG 862
Qy 848 CAGCTAACGCAATAAGTAGACCGCTGGGAGTAGCGCGCAAGGTTTAAAACTCAAATGA 907
Db 863 CAGCTAACGCAATAAGTAGACCGCTGGGAGTAGCGCGCAAGGTTTAAAACTCAAATGA 922
Qy 908 ATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAA 967
Db 923 ATTGACGGGGCCCGCACAAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAA 982
Qy 968 CTTTACCTGCTTGTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCCTTGG 1022
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```
RESULT 12
AB016054 AB016054 1536 bp DNA linear BCT 10-MAY-2000
LOCUS Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
DEFINITION strain:NIBH P2J2.
ACCESSION AB016054
VERSION AB016054.1 GI:6691635
KEYWORDS 16S ribosomal RNA.
SOURCE Psychrobacter pacificensis
ORGANISM Psychrobacter pacificensis
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Db	974	CCGGTCTTGACATACACAGAACTCTGTAGAGATACAGAGATGCTTCGCGAAATTGTGATA	1033
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Db	1034	CAGGTGCTGCATGGCTGTTCGTCACTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACG	1093
Qy	1094	AGCGCAACCTTGTCTCTTAGTTACCAGC	1121
Db	1094	AGCGCAACCTTGTCTCTTAGTTACCAGC	1121
RESULT 13			
AP505739			
LOCUS	AP505739	1425 bp	DNA linear BCT 31-JAN-2003
DEFINITION	Bacterium UMB10E 16S ribosomal RNA gene, partial sequence.		
ACCESSION	AP505739		
VERSION	AP505739.1	GI:28173016	
KEYWORDS	bacterium UMB10E		
SOURCE	bacterium UMB10E		
ORGANISM	Bacteria.		
REFERENCE	1 (bases 1 to 1425)		
AUTHORS	Tang,R.J. and Cooney,J.J.		
TITLE	Tributylin-resistant, biofilm-forming bacteria isolated from Boston Harbor, MA		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1425)		
AUTHORS	Tang,R.J. and Cooney,J.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-APR-2002) Environmental, Coastal and Ocean Sciences, University of Massachusetts Boston, 100 Morrissey Blvd., Boston, MA 02125-3393, USA		
FEATURES			
source	Location/Qualifiers		
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	/mol_type="genomic DNA"		
	/strain="UMB10E"		
	/isolation_source="Boston Harbor surface water"		
	/db_xref="taxon:206003"		
	/environmental_sample		
	/country="USA: Massachusetts"		
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	<1..>1425		
	/product="16S ribosomal RNA"		
ORIGIN			
Query Match	37.1%;	Score 566;	DB 1; Length 1425;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches	616; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
Qy	371	AACCTTGATCCAGCCATCGCGGTGTGCAAGAAAGCCCTTTTGGTTGTAAAGCACATTTAA	430
Db	325	AACCTTGATCCAGCCATCGCGGTGTGCAAGAAAGCCCTTTTGGTTGTAAAGCACATTTAA	384
Qy	431	GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCATGACATTAGTCGCAATAAGC	490
Db	385	GCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCATGACATTAGTCGCAATAAGC	444
Qy	491	ACCGGTAACTCTGTCCACAGCCCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAAT	550
Db	445	ACCGGTAACTCTGTCCACAGCCCGCGGTAAATACAGAGGGTGCAGCGTTAATCGGAAT	504
Qy	551	TACTGGCGGTAAAGCAGCGGTAGTGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	610
Db	505	TACTGGCGGTAAAGCAGCGGTAGTGGCTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	564
Qy	611	ACCTGGGAACCTGCATCTGAAACTGTTTAGCTAGAGTAGGTAGAGAGGGAAGTAGAATTTCA	670
Db	565	ACCTGGGAACCTGCATCTGAAACTGTTTAGCTAGAGTAGGTAGAGAGGGAAGTAGAATTTCA	624
Qy	671	GGTGTAGCGGTGAATGCGGTAGAGATCTGAAGAAATACCGATGGCGAAGCAGCTTCCTG	730
Db	625	GGTGTAGCGGTGAATGCGGTAGAGATCTGAAGAAATACCGATGGCGAAGCAGCTTCCTG	684



	Matches	616;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	371	AACCTCTGATCCAGCCATCCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAA	430							
Db	329	AACCTCTGATCCAGCCATCCGCGTGTGTGAAGAAGCCCTTTTGGTTGTAAAGCACTTTAA	388							
Qy	431	GCAGTGAAGAAGACTCTTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGATAAGC	490							
Db	389	GCAGTGAAGAAGACTCTTTCGGTTAATACCCGGAGACGATGACATTAGCTGCAGATAAGC	448							
Qy	491	ACCGGCTAACTCTGTGCCAGAGCCGCGTGAATACAGAGGGTGCAGCGTTAATCGGAAT	550							
Db	449	ACCGGCTAACTCTGTGCCAGAGCCGCGTGAATACAGAGGGTGCAGCGTTAATCGGAAT	508							
Qy	551	TACTGGGCGTAAAGCGAGCGTAGGTGGCTTGATAGTCAGATGTGAAATCCCGGGCTTA	610							
Db	509	TACTGGGCGTAAAGCGAGCGTAGGTGGCTTGATAGTCAGATGTGAAATCCCGGGCTTA	568							
Qy	611	ACCTGGGAATGCTGATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGGAAGTAGAATTCA	670							
Db	569	ACCTGGGAATGCTGATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGGAAGTAGAATTCA	628							
Qy	671	GGTGTAGCGGTCAATCGTAGAGATCTGAAGGATACCGATGGCGRAGGCAGCTTCCTG	730							
Db	629	GGTGTAGCGGTCAATCGTAGAGATCTGAAGGATACCGATGGCGRAGGCAGCTTCCTG	688							
Qy	731	GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCCTGGT	790							
Db	689	GCATCATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAACAGGATTAGATACCCCTGGT	748							
Qy	791	AGTCCACCCCGTAAACGATGTCTACTAGTCGTGGGTCCCTTGAGGACTTATGTAACGCAG	850							
Db	749	AGTCCACCCCGTAAACGATGTCTACTAGTCGTGGGTCCCTTGAGGACTTATGTAACGCAG	808							
Qy	851	CTAACGCAATAAGTAGACCGCTCGGGAGTAGCGGCCCAAGTTAAACTCAATGAATT	910							
Db	809	CTAACGCAATAAGTAGACCGCTCGGGAGTAGCGGCCCAAGTTAAACTCAATGAATT	868							
Qy	911	GACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTGATGCAACGCGAAGAACCT	970							
Db	869	GACGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTGATGCAACGCGAAGAACCT	928							
Qy	971	TACCTGGTCTTGACATA	987							
Db	929	TACCTGGTCTTGACATA	945							

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Job time : 6693 secs

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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:00:33 ; Search time 870 Seconds  
(without alignments)  
10383.362 Million cell updates/sec

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Perfect score: 1526  
Sequence: 1 ttgatcatgctccagatt.....acctgcgctggtgatcaactc 1526

Scoring table: OLIGO\_NUC3  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 9: geneseqn2003bs:\*
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- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526	100.0	1526	4	AAC87531 Psychroba
2	136	8.9	1485	2	Aaql3256 16S rRNA
3	136	8.9	269223	4	Aaf28554 Genomic f
4	121	7.9	549	3	Aac95222 Cat flea
5	121	7.9	1487	5	Aas11034 Shigella
6	121	7.9	1489	6	Abst1622 Klebsiell
7	121	7.9	1506	6	Abst1613 Escherich
8	121	7.9	1533	13	Aqg81656 Enterobac
9	121	7.9	1534	10	Adb61683 16S rRNA
10	121	7.9	1540	1	Aan91514 Escherich
11	121	7.9	1542	2	Aat29140 rRNA gene
12	121	7.9	1542	4	Aac62270 Escherich
13	121	7.9	1542	5	Aaf23015 E. coli 1
14	121	7.9	1542	5	Aah75410 E. coli 1
15	121	7.9	1542	6	Abn85800 Escherich
16	121	7.9	1542	9	Adb16299 Cleavase
17	121	7.9	1542	9	Aad57988 Escherich
18	121	7.9	1542	10	Adc02547 E. coli r
19	121	7.9	1542	12	Aqdl6352 Nucleotid
20	121	7.9	1549	3	Aaa65897 E. coli p

21	121	7.9	1549	3	AAA66050	Aaa66050 E. coli p
22	121	7.9	1549	3	AAA66055	Aaa66055 E. coli p
c 23	121	7.9	5090	2	Aax24988	Aax24988 E. coli M
24	121	7.9	5097	2	Aax24983	Aax24983 E. coli M
25	121	7.9	5098	2	Aax24984	Aax24984 E. coli M
26	121	7.9	5105	2	Aax24989	Aax24989 E. coli M
c 27	121	7.9	5341	2	Aax24986	Aax24986 E. coli M
c 28	121	7.9	7508	9	AAL62713	Aal62713 Escherich
c 29	121	7.9	10903	12	ADK51929	Adk51929 Novel rRN
c 30	121	7.9	11918	12	ADK51930	Adk51930 Novel rRN
31	121	7.9	13278	12	ADK51931	Adk51931 Novel rRN
32	116	7.6	1462	4	Aaf85587	Aaf85587 Pseudoalt
33	116	7.6	1474	6	Aai17194	Aai17194 Pseudoalt
34	116	7.6	1492	13	ADS52325	Ads52325 Pseudoalt
35	116	7.6	1494	8	ABX16332	Abx16332 Aliphatic
36	116	7.6	1528	2	AAx83570	Aax83570 16S rDNA
37	116	7.6	1529	2	AAx83564	Aax83564 16S rDNA
38	116	7.6	1529	2	AAx83566	Aax83566 16S rDNA
39	116	7.6	1529	2	AAx83565	Aax83565 16S rDNA
40	116	7.6	1529	2	AAx83567	Aax83567 16S rDNA
41	116	7.6	1535	2	AAx83568	Aax83568 16S rDNA
42	116	7.6	1535	2	AAx83569	Aax83569 16S rDNA
43	115	7.5	888	2	AAQ46120	Aaq46120 E. coli 1
44	115	7.5	1542	2	AAQ46119	Aaq46119 E. coli 1
45	114	7.5	1541	5	AA511022	Aaa511022 Salmonell

## ALIGNMENTS

## RESULT 1

AAC87531  
ID AAC87531 standard; DNA; 1526 BP.  
XX  
AC AAC87531;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Psychrobacter pacificensis NIBH P2K6 16S rDNA, SEQ ID NO:1.  
XX  
KW 16S rDNA; species-specific detection; identification;  
KW psychrophilic bacterium; oceanic circulation; Psychrobacter;  
KW strain NIBH P2K6; ds.  
XX  
OS Psychrobacter pacificensis.  
XX  
PN WO200071705-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 25-MAY-2000; 2000WO-JP003372.  
XX  
PR 25-MAY-1999; 99JP-00145342.  
XX  
PA 30-MAR-2000; 2000WO-JP002045.  
XX  
(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
XX  
PI Maruyama A, Kitamura K, Kurane R;  
XX  
DR WPI; 2001-025158/03.  
XX  
PT DNA probe originating from psychrotrophic bacterium applicable in species  
PT -specific detection of the microorganism as indication in studying and  
PT monitoring its growth and circulation of deep-sea water with sensitivity.  
XX  
PS Claim 1; Page 30; 37pp; Japanese.  
XX  
CC The invention relates to a 1526 bp Psychrobacter pacificensis 16S rDNA  
CC sequence (AAC87531) and an oligonucleotide probe (AAC87532) comprising  
CC part of the Psychrobacter pacificensis 16S rDNA sequence which are used  
CC for monitoring the growth of psychrophilic bacteria and the circulation  
CC of deep-sea water. Psychrobacter pacificensis is an aerobic, Gram-  
CC negative, non-motile, non-spore-forming oxidase-positive bacterium

CC originally isolated from the Japan Trench. The invention also relates to  
CC a novel method for detecting or specifically identifying Psychrobacter  
CC pacificensis, Psychrobacter glacincola, and related species, or  
CC Psychrobacter pacificensis only via the use of the 16S rDNA sequence. The  
CC 16S rDNA sequence and derived oligonucleotide probe are useful for the  
CC species-specific detection of Psychrobacter pacificensis to study and  
CC monitor its growth as an indicator of the circulation of deep-sea water.  
CC The method of the invention is rapid, accurate and has high sensitivity,  
CC and removes the need to separate and culture the biological materials.  
CC The present sequence represents the Psychrobacter pacificensis 16S rDNA  
XX  
SQ Sequence 1526 BP; 401 A; 332 C; 467 G; 323 T; 0 U; 3 Other;

Query Match 100.0%; Score 1526; DB 4; Length 1526;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGATCATGCTCCAGATTGAACGACTGGCGGCGAGGCTTAACACATGCAAGTCGAGCG 60  
DB 1 TTTGATCATGCTCCAGATTGAACGACTGGCGGCGAGGCTTAACACATGCAAGTCGAGCG 60  
QY 61 GAAACGATGATAGCTTCTATTAGGCTCGAGNCGCGGAGGCTGAGTAACTTAGGA 120  
DB 61 GAAACGATGATAGCTTCTATTAGGCTCGAGNCGCGGAGGCTGAGTAACTTAGGA 120  
QY 121 ATCTACCTAGTAGTGGGGATAGCTCGGGGAAACTCGAATTAATACCGCATAGCTCTACG 180  
DB 121 ATCTACCTAGTAGTGGGGATAGCTCGGGGAAACTCGAATTAATACCGCATAGCTCTACG 180  
QY 181 GGAGAAAGCAGGGGNTCAATAGACCTTGCCTATTAGATGAGCTTAAGTCGGATTAGCTA 240  
DB 181 GGAGAAAGCAGGGGNTCAATAGACCTTGCCTATTAGATGAGCTTAAGTCGGATTAGCTA 240  
QY 241 GATGGTGGGTAAAGGCTTACCATTGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAG 300  
DB 241 GATGGTGGGTAAAGGCTTACCATTGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAG 300  
QY 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGGAGGAGCAGGATGGGGAATATGGA 360  
DB 301 CCACACGGGACTGAGACACGGCCCGGACTCTACGGGAGGAGCAGGATGGGGAATATGGA 360  
QY 361 CAATGNGGGAAACCTCATCCAGCCATCCGCGGTGTGAAGAGGCTTTGGTGTAA 420  
DB 361 CAATGNGGGAAACCTCATCCAGCCATCCGCGGTGTGAAGAGGCTTTGGTGTAA 420  
QY 421 AGCACTTTAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCAGATGACATTAGCTG 480  
DB 421 AGCACTTTAAGCAGTGAAGAAGACTCTTCGGTTAATACCCGGGAGCAGATGACATTAGCTG 480  
QY 481 CAGNATTAAGCAGCGGCTAACTCTGTGCGAGGCGCGGCTTAATACAGAGGCTGCGAGCGT 540  
DB 481 CAGNATTAAGCAGCGGCTAACTCTGTGCGAGGCGCGGCTTAATACAGAGGCTGCGAGCGT 540  
QY 541 TAATCGGAATTTACTGGCGCTAAAGCAGCGTAGTGGCTTGAATGATGATGAATC 600  
DB 541 TAATCGGAATTTACTGGCGCTAAAGCAGCGTAGTGGCTTGAATGATGATGAATC 600  
QY 601 CCCGGGCTTAACCTGGGAACTGCACTCTGAACTGTTAGGCTAGAGTAGGTGAGAGGGAAG 660  
DB 601 CCCGGGCTTAACCTGGGAACTGCACTCTGAACTGTTAGGCTAGAGTAGGTGAGAGGGAAG 660  
QY 661 TAGAATTCAGGTGATAGCGGTAAATCGGTAGAGATCTGAAGGAATACCGATGCGGAAGG 720  
DB 661 TAGAATTCAGGTGATAGCGGTAAATCGGTAGAGATCTGAAGGAATACCGATGCGGAAGG 720  
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DB 721 CAGCTCTCGCATCACTGACACTGAGGCTCGAAGCGTGGGTAGCAACACAGATTAG 780  
QY 781 ATACCTCGGTAGTCCACCGCGTAAACGATGCTACTAGTGGTGGTCCCTTAGGACTT 840  
DB 781 ATACCTCGGTAGTCCACCGCGTAAACGATGCTACTAGTGGTGGTCCCTTAGGACTT 840

QY 841 AGTGACGCGAGCTAAACCAATAAGTACACGCGCTGGGAGGTACGCGCGAAGGTAAACT 900  
DB 841 AGTGACGCGAGCTAAACCAATAAGTACACGCGCTGGGAGGTACGCGCGAAGGTAAACT 900  
QY 901 CAAATGAATTTGACGCGGGGCGGCAACGCGGTGAGCATGTGTTTAATTCGATGCAACG 960  
DB 901 CAAATGAATTTGACGCGGGGCGGCAACGCGGTGAGCATGTGTTTAATTCGATGCAACG 960  
QY 961 CGAAGAACCTTACCTGCTTGTGATACACAGAACTCTTGTAGAGATACGAGATGCGCTTC 1020  
DB 961 CGAAGAACCTTACCTGCTTGTGATACACAGAACTCTTGTAGAGATACGAGATGCGCTTC 1020  
QY 1021 GGGAAATTGTGATACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
DB 1021 GGGAAATTGTGATACAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
QY 1081 AAGTCCCGCAACGAGCGCAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140  
DB 1081 AAGTCCCGCAACGAGCGCAACCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140  
QY 1141 AGGATATGCTGCTGATGACAACTGGAGGAGGCGGAGCGAGCTCAAGTCAATGCGCCT 1200  
DB 1141 AGGATATGCTGCTGATGACAACTGGAGGAGGCGGAGCGAGCTCAAGTCAATGCGCCT 1200  
QY 1201 TAGCACCAGGCTACACAGCTGCTCAATGCTAGGTACAGAGGCGAGCTACACAGCGATG 1260  
DB 1201 TAGCACCAGGCTACACAGCTGCTCAATGCTAGGTACAGAGGCGAGCTACACAGCGATG 1260  
QY 1261 TGATGGGAATCTCAAAAGGCTATCTGCTAGTCCAGATTTGGAGTCTGCAACTCGATCCATG 1320  
DB 1261 TGATGGGAATCTCAAAAGGCTATCTGCTAGTCCAGATTTGGAGTCTGCAACTCGATCCATG 1320  
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DB 1321 AAGTAGAATCGCTAGTAACTCGCGGATCAGAAATCGCGCGTGAATAGCTTCCCGGGCCTT 1380  
QY 1381 GTACACACGCGCGCTCACACATGGGAGTTGATTCACACAGAAAGTGGTTAGCCCTAACTTA 1440  
DB 1381 GTACACACGCGCGCTCACACATGGGAGTTGATTCACACAGAAAGTGGTTAGCCCTAACTTA 1440  
QY 1441 GTGAGGCGGATCACACGCTGCTGATGATCGAGTGGGTTGAAGTCGTAACAGGTAGCCGT 1500  
DB 1441 GTGAGGCGGATCACACGCTGCTGATGATCGAGTGGGTTGAAGTCGTAACAGGTAGCCGT 1500  
QY 1501 AGGGGAACCTGCGGCTGGATCACCTC 1526  
DB 1501 AGGGGAACCTGCGGCTGGATCACCTC 1526

## RESULT 2

AAQ13256  
ID AAQ13256 standard; DNA; 1485 BP.

XX AAQ13256;

XX AC AC

XX 24-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 25-OCT-1991 (first entry)

XX XX

XX DE DE

XX 16S rRNA gene (partial).

XX KW Probe; detection; Moraxella; Neisseria; 23S; ribosomal RNA; ss.

XX OS Moraxella catarrhalis; ITG 4197.

XX PN WO9111531-A.

XX PD 08-AUG-1991.

XX XX

XX 02-FEB-1990; 90EP-00400297.

XX 02-FEB-1990; 90EP-00400297.

XX PR

XX XX

PA (INNO-) INNOGENETICS NV SA.  
XX Roseau R, Vanheuvens H;  
XX WPI; 1991-252662/34.  
XX Nucleic acid probes for selective detection of brachyella catarrhalis -  
PT can detect bacterial -RNA or DNA and differentiate it from other  
PT bacteria.  
XX Disclosure; Fig 1(A); 41pp; English.  
PS  
XX This sequence was used to derive the probes BC1-BC5 as represented in  
CC AAQ13258-67. Probes BC9 as represented in AAQ13268-69 are derived from  
CC the 23S rRNA gene (AAQ13257). (Updated on 25-MAR-2003 to correct PI  
CC field.) (Updated on 24-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 1485 BP; 390 A; 325 C; 449 G; 320 T; 0 U; 1 Other;  
  
Query Match 8.9%; Score 136; DB 2; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 2.5e-60;  
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 852 TAACGCAATAAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTG 911  
Db  
QY 912 ACGGGGGCCCGCACAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTT 971  
Db 869 ACGGGGGCCCGCACAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTT 928  
QY 972 ACCTGGTCTTGACATA 987  
Db 929 ACCTGGTCTTGACATA 944  
  
RESULT 3  
ID AAF28554/c  
XX AAF28554 standard; DNA; 269223 BP.  
AC AAF28554;  
XX  
DT 04-APR-2001 (first entry)  
XX  
DE Genomic fragment #41.  
XX  
KW Genomic library; bacteria; human upper airway; otitis media; sinusitis;  
KW bronchopulmonary; endocarditis; meningitis; ss.  
XX  
OS Moraxella catarrhalis.  
XX  
PN WO200078968-A2.  
XX  
PD 28-DEC-2000.  
XX  
PF 16-JUN-2000; 2000WO-US016649.  
XX  
PR 18-JUN-1999; 99US-0140121P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Lagace RE, Patterson C, Berg KL;  
XX  
DR WPI; 2001-041427/05.  
XX  
PT Genomic library for identifying diagnostic and therapeutic compositions,  
PT and for identifying virulence factors, regulatory elements and drug  
PT targets, comprises Moraxella catarrhalis nucleic acids.  
XX  
XX Claim 1; Page 486-545; 545pp; English.  
PS  
XX The present invention relates to a Moraxella catarrhalis genomic library  
CC comprising of a combination of 41 nucleic acid molecules (see AAF28514-  
CC

CC AAF28554). The library has a number of uses described in the  
CC specification e.g. is useful for identifying diagnostic and therapeutic  
CC compositions. M. catarrhalis (Branhamella catarrhalis) is a large  
CC aerobic, gram-negative diplococcus, normally found among the bacterial  
CC flora of human upper airways. M. catarrhalis is known to cause acute,  
CC localised infections such as otitis media, sinusitis and bronchopulmonary  
CC infection and life-threatening, systemic diseases including endocarditis  
CC and meningitis  
XX  
SQ Sequence 269223 BP; 77067 A; 56596 C; 57380 G; 78180 T; 0 U; 0 Other;  
  
Query Match 8.9%; Score 136; DB 4; Length 269223;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 852 TAACGCAATAAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTG 911  
Db 92136 TAACGCAATAAGTAGACCGCTGGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTG 92077  
  
QY 912 ACGGGGGCCCGCACAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTT 971  
Db 92076 ACGGGGGCCCGCACAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTT 92017  
  
QY 972 ACCTGGTCTTGACATA 987  
Db 92016 ACCTGGTCTTGACATA 92001  
  
RESULT 4  
ID AAC95222  
XX AAC95222 standard; cDNA; 549 BP.  
AC AAC95222;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE Cat flea head and nerve cord (HNC) cDNA, SEQ ID NO:1717.  
XX  
KW Cat flea; head and nerve cord nucleic acid; HNC; flea infestation;  
KW vaccine; antiparasitic; therapeutic target; diagnosis; detection; ss.  
XX  
OS Ctenocephalides felis.  
XX  
PN WO200061621-A2.  
XX  
PD 19-OCT-2000.  
XX  
PF 07-APR-2000; 2000WO-US009437.  
XX  
PR 09-APR-1999; 99US-0128704P.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;  
XX  
DR WPI; 2000-656323/63.  
XX  
PT Flea Malpighian tubule and head and nerve cord tissue derived nucleic  
PT acids useful for the prevention, diagnosis and treatment of flea  
PT infestations.  
XX  
PS Claim 26; Page 820; 964pp; English.  
XX  
CC The invention relates to novel cat flea (Ctenocephalides felis) nucleic  
CC acids which are expressed in hindgut and Malpighian tubule (HMT) tissue  
CC or head and nerve cord (HNC) tissue. The invention also relates to the  
CC encoded proteins. The invention additionally encompasses expression  
CC constructs, recombinant viruses and recombinant cells comprising the  
CC nucleic acids of the invention, recombinant production of the proteins,  
CC antibodies against the proteins, a method of identifying inhibitors of  
CC the proteins, and compositions comprising the inhibitors for  
CC administration to an animal. The nucleic acids, and the proteins they  
CC encode may be used in the prevention, treatment and diagnosis of diseases

CC associated with flea infestations. For example, the nucleic acids may be  
 CC used to produce an HMT or HNC protein according to standard recombinant  
 CC DNA methodology by inserting the nucleic acids into a host cell and  
 CC culturing the cell to express the protein. The HMT and HNC nucleic acids  
 CC may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect  
 CC and quantitate the presence of cat flea or other homologous nucleic acid  
 CC sequences in samples. They may also be used to study the expression and  
 CC function of the proteins and their role in metabolism. The HMT and HNC  
 CC proteins may be used as antigens in the production of specific  
 CC antibodies, and in assays to identify modulators (agonists and  
 CC antagonists) of HMT and/or HNC protein expression and activity. The anti-  
 CC HMT/HNC protein antibodies and antagonists may also be used to  
 CC downregulate protein expression and activity. The antibodies may also be  
 CC used as diagnostic agents for detecting the presence of flea polypeptides  
 CC in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The  
 CC present sequence represents a cat flea HNC cDNA of the invention  
 XX  
 SQ Sequence 549 BP; 132 A; 131 C; 173 G; 112 T; 0 U; 1 Other;

Query Match 7.9%; Score 121; DB 3; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 866 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTGACGGGGGCCGCGAC 925  
 DB 163 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTGACGGGGGCCGCGAC 222  
 QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 985  
 DB 223 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 282  
 QY 986 T 986  
 DB 283 T 283

RESULT 5  
 AAS11034  
 ID AAS11034 standard; DNA; 1487 BP.  
 XX  
 AC AAS11034;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 24-OCT-2001 (first entry)  
 XX  
 XX Shigella dysenteriae 16s ribosomal RNA gene.  
 XX Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection; human;  
 KW food grain supplement; livestock; poultry; therapeutic; ds.  
 XX Shigella dysenteriae.  
 OS WO200142457-A2.  
 XX  
 FN 14-JUN-2001.  
 PD  
 XX 29-NOV-2000; 2000WO-US042391.  
 PF  
 XX 29-NOV-1999; 99US-0168150P.  
 PR  
 XX (AVTB-) AVI BIOPHARMA INC.  
 PA  
 XX Iversen PL;  
 FI  
 XX WPI; 2001-457295/49.  
 XX  
 XX Antibacterial compound, useful for treating bacterial infections and as  
 PT livestock and poultry food supplement, comprises antisense  
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.  
 XX  
 XX Disclosure; Page; 62pp; English.  
 PS  
 XX AAS11021-AAS11034 represent the coding sequences of bacterial 16s  
 CC

CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-  
 CC bacterial compounds comprising substantially uncharged antisense  
 CC oligomers containing 8-40 nucleotide subunits, including a targeting  
 CC nucleic acid sequence at least 10 nucleotides in length which is  
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The  
 CC antisense oligomers are used for treating a bacterial infection in a  
 CC human or a mammalian animal produced by *Escherichia coli*, *Salmonella*  
 CC typhimurium, *Pseudomonas aeruginosa*, *Vibrio cholera*, *Neisseria*  
 CC gonorrhoea, *Helicobacter pylori*, *Bartonella henselae*, *Haemophilus*  
 CC influenza, *Shigella dysenteriae*, *Staphylococcus aureus*, *Mycobacterium*  
 CC tuberculosis, *Streptococcus pneumoniae*, *Treponema pallidum* and *Chlamydia*  
 CC trachomatis. The antibacterial compound may be used as a food grain  
 CC supplement in livestock and poultry food composition. Note: The present  
 CC sequence is not shown in the specification but has been accessed from  
 CC GenBank using the appropriate accession number given in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 1487 BP; 375 A; 341 C; 472 G; 299 T; 0 U; 0 Other;

Query Match 7.9%; Score 121; DB 5; Length 1487;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 866 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTGACGGGGGCCGCGAC 925  
 DB 857 GACGCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTGACGGGGGCCGCGAC 916  
 QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 985  
 DB 917 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGGCGAAGAACCTTACCTGGTCTTGACA 976  
 QY 986 T 986  
 DB 977 T 977

RESULT 6  
 ABS71622  
 ID ABS71622 standard; DNA; 1489 BP.  
 XX  
 AC ABS71622;  
 XX  
 DT 28-NOV-2002 (first entry)  
 DT  
 DE Klebsiella pneumoniae 16S RNA.  
 XX  
 KW Eubacteria; species detection; speciation; 16s RNA; gene; ss.  
 XX Klebsiella pneumoniae.  
 OS WO200270728-A2.  
 XX  
 FN 12-SEP-2002.  
 PD  
 XX 01-MAR-2002; 2002WO-US006050.  
 XX  
 PF 01-MAR-2001; 2001US-0272642P.  
 PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 XX Rothman RE, Yang S, Lin S, Kelen GD;  
 PI WPI; 2002-698755/75.  
 DR  
 XX Detecting and determining species source of eubacterial DNA in a sample,  
 PT comprises amplifying template DNA in the sample using a real-time  
 PT polymerase chain reaction with the use of primers and at least two  
 PT fluorogenic probes.  
 XX  
 XX Example 1; Page; 39pp; English.  
 PS  
 XX The invention describes a method of detecting and determining species  
 CC source of eubacterial DNA in a sample. The method comprises amplifying  
 CC

CC template DNA in the sample using a real-time polymerase chain reaction (R  
CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
CC least two fluorogenic probes. The methods are useful in detecting and  
CC determining species source of eubacterial DNA in a sample. The present  
CC method allows for highly sensitive detection of any eubacterial species  
CC with simultaneous speciation. It eliminates false positive results in  
CC detecting bacterial infections. This sequence represents a bacterial 16S  
CC RNA gene used to create the primers of the invention

XX SQ Sequence 1489 BP; 375 A; 341 C; 475 G; 294 T; 0 U; 4 Other;

Query Match 7.9%; Score 121; DB 6; Length 1489;  
Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCAAGGTTAAATCAATGAATTAATGACGGGGCCCGCAC 925  
DB 846 GACCGCTGGGAGTACGCCCAAGGTTAAATCAATGAATTAATGACGGGGCCCGCAC 905

QY 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 985  
DB 906 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 965

QY 986 T 986  
DB 966 T 966

RESULT 7  
ABS71613  
ID ABS71613 standard; DNA; 1506 BP.

XX AC ABS71613;  
XX DT 28-NOV-2002 (first entry)  
XX DE Escherichia coli 16S RNA.  
XX KW Eubacteria; species detection; speciation; 16S RNA; gene; ss.  
XX OS Escherichia coli.  
XX PN WO200270728-A2.  
XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US006050.  
XX PR 01-MAR-2001; 2001US-0272642P.  
XX PA (UYJO ) UNIV JOHNS HOPKINS.  
XX PI Rothman RE, Yang S, Lin S, Kelen GD;  
XX WPI; 2002-698755/75.

XX Detecting and determining species source of eubacterial DNA in a sample,  
XX comprises amplifying template DNA in the sample using a real-time  
XX polymerase chain reaction with the use of primers and at least two  
XX fluorogenic probes.

XX Example 1; Page; 39pp; English.  
XX The invention describes a method of detecting and determining species  
XX source of eubacterial DNA in a sample. The method comprises amplifying  
XX template DNA in the sample using a real-time polymerase chain reaction (R  
XX -T PCR), where the PCR or PCR reaction mixture comprises primers and at  
XX least two fluorogenic probes. The methods are useful in detecting and  
XX determining species source of eubacterial DNA in a sample. The present  
XX method allows for highly sensitive detection of any eubacterial species  
XX with simultaneous speciation. It eliminates false positive results in  
XX detecting bacterial infections. This sequence represents a bacterial 16S  
XX RNA gene used to create the primers of the invention

XX SQ Sequence 1506 BP; 378 A; 346 C; 481 G; 301 T; 0 U; 0 Other;

Query Match 7.9%; Score 121; DB 6; Length 1506;  
Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCAAGGTTAAATCAATGAATTAATGACGGGGCCCGCAC 925  
DB 857 GACCGCTGGGAGTACGCCCAAGGTTAAATCAATGAATTAATGACGGGGCCCGCAC 916

QY 926 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 985  
DB 917 AAGCGTGGAGCATGTGTTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTGACA 976

QY 986 T 986  
DB 977 T 977

RESULT 8  
ADQ81656  
ID ADQ81656 standard; DNA; 1533 BP.

XX AC ADQ81656;  
XX DT 21-OCT-2004 (first entry)  
XX DE Enterobacter sp. C-1 strain 16S rRNA gene SeqID 1.  
XX KW microorganism; 16S rRNA; ds; water soluble polysaccharide; fucose;  
XX KW galactose; glucose; glucuronic acid; anti-cancer;  
XX KW 4,5-dihydroxy 2-cyclopentene-1-one; DHCP; food; paper diaper.

XX OS Enterobacter sp.  
XX PN JP2004208563-A.  
XX PD 29-JUL-2004.

XX PF 27-DEC-2002; 2002JP-00380990.  
XX PR 27-DEC-2002; 2002JP-00380990.  
XX PA (ASAH ) ASahi KASEI KK.  
XX WPI; 2004-538189/52.

XX Novel microorganism having 16S rRNA gene, useful for producing water-  
XX soluble polysaccharide which produces anti-cancer substance on heating  
XX for long time.  
XX Claim 1; SEQ ID NO 1; 15pp; Japanese.

XX This invention relates to a novel microorganism having a 16S rRNA gene  
XX comprising a fully defined sequence of 1533 nucleotides. Specifically, it  
XX refers to a water soluble polysaccharide producing microbe identified as  
XX Enterobacter sp. C-1 (FERM P-18947). The present invention describes the  
XX water soluble polysaccharide as comprising fucose, galactose, glucose and  
XX glucuronic acid, and collection of the same involves altering the pH  
XX value of the microbial culture solution to pH 4 by adding long-chain  
XX quaternary ammonium salt in order to isolate the ammonium salt  
XX precipitate of the polysaccharide. Accordingly, this microorganism is  
XX useful for producing water-soluble polysaccharides that in turn can be  
XX used to produce the anti-cancer substance 4,5-dihydroxy 2-cyclopentene-1-  
XX one (DHCP). Furthermore, the water-soluble polysaccharide compositions  
XX are useful in food and paper diaper products. This polynucleotide  
XX sequence is the Enterobacter sp. C-1 strain 16S rRNA gene of the  
XX invention.

XX SQ Sequence 1533 BP; 383 A; 354 C; 489 G; 307 T; 0 U; 0 Other;  
XX Query Match 7.9%; Score 121; DB 13; Length 1533;



Query Match 7.9%; Score 121; DB 1; Length 1540;  
 Best Local Similarity 80.2%; Pred. No. 1.8e-52;  
 Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGAGTACGCGCCAGGTTAAATCTCAATGAATTCAGCGGGGCCCGCAC 925  
 DB 876 GACCGCTGGAGTACGCGCCAGGTTAAATCTCAATGAATTCAGCGGGGCCCGCAC 935

QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGCTCTTGACA 985  
 DB 936 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGCTCTTGACA 995

QY 986 T 986  
 DB 996 U 996

RESULT 11  
 AAT29140  
 ID AAT29140 standard; DNA; 1542 BP.  
 AC AAT29140;  
 DT 02-DEC-1996 (first entry)  
 DE rRNA gene (rrsE) from *Escherichia coli*.  
 KW p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;  
 KW *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;  
 KW *Staphylococcus*; identification; detection; ds.  
 XX *Escherichia coli*.  
 OS WO9615267-A1.  
 PN 23-MAY-1996.  
 PD 09-NOV-1995; 95WO-US014673.  
 PF 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PA Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;  
 PI Fors L, Olive DW;  
 DR WPI; 1996-259862/26.  
 XX  
 CC Cleavage of nucleic acids to detect mutation(s) - allows detection esp.  
 CC in human p53 gene, to identify strains of microorganisms and viruses.  
 PT Example 34; Page 314; 433pp; English.  
 PS  
 CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected  
 CC from the group consisting of cleavage (RTM) BN enzyme, *Thermus aquaticus*  
 CC DNA polymerase, *Thermus thermophilus* DNA polymerase, *Escherichia coli*  
 CC ExoII and the *Saccharomyces cerevisiae* Radi/Radi complex. The nucleic  
 CC acid substrate is preferably an oligonucleotide containing a human p53  
 CC gene sequence or alternatively, microbial gene sequences. Cleavage  
 CC products are compared to the cleavage products of reference gene  
 CC sequences. The method is used for detecting mutation in the human p53  
 CC gene; for identifying strains of microorganisms, especially bacteria  
 CC selected from the group of members of the genera *Campylobacter*,  
 CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*. The  
 CC method may also be used for the identification of viruses, especially  
 CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Seven  
 CC primers (AAT29133-39) were used to amplify 16S rRNA genes. The amplified  
 CC genes were then subjected to the cleavage method and the resulting  
 CC fragmentation patterns used in identification of the microorganisms from

CC which the rRNA genes originated. 16S rRNA genes are given in AAT29140-42  
 XX Sequence 1542 BP; 389 A; 352 C; 487 G; 314 T; 0 U; 0 Other;  
 SQ

Query Match 7.9%; Score 121; DB 2; Length 1542;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGAGTACGCGCCAGGTTAAATCTCAATGAATTCAGCGGGGCCCGCAC 925  
 DB 877 GACCGCTGGAGTACGCGCCAGGTTAAATCTCAATGAATTCAGCGGGGCCCGCAC 936

QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGCTCTTGACA 985  
 DB 937 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACCTGCTCTTGACA 996

QY 986 T 986  
 DB 997 T 997

RESULT 12  
 AAC62270  
 ID AAC62270 standard; DNA; 1542 BP.  
 AC AAC62270;  
 DT 19-MAR-2001 (first entry)  
 DE *Escherichia coli* reference 16S rDNA sequence.  
 XX 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;  
 KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;  
 KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.  
 XX *Escherichia coli*.  
 OS WO200063443-A2.  
 PN 26-OCT-2000.  
 PD 13-APR-2000; 2000WO-US009883.  
 PF 15-APR-1999; 99US-0129511P.  
 PR (DUPO) DU PONT DE NEMOURS & CO E I.  
 PA Hendrickson ER, Ebersole RC;  
 PI WPI; 2001-024581/03.  
 DR  
 XX New 16S rDNA profile derived from Dehalococcoides ethenogenes and  
 PT indicative of a dechlorinating bacterial strain.  
 XX Disclosure; Page 55; 55pp; English.  
 PS  
 CC The present sequence represents a reference 16S rDNA sequence. The  
 CC specification describes 16S rDNA sequences, derived from various strains  
 CC of Dehalococcoides ethenogenes. These 16S rDNA profile is linked to  
 CC dechlorinating activity. Bacterial strain comprising the 16S rDNA  
 CC sequence of the invention are useful for the dechlorination of  
 CC chlorinated compounds such as carbontetrachloride, tetrachloroethane,  
 CC chloroform, dichloromethane, trichloroethane, dichloroethylene, vinyl  
 CC chloride, and chloroformatics. The 16S rDNA sequence is also useful for  
 CC identification of new chlorinating bacteria, as well as sub-typing  
 CC strains of Dehalococcoides ethenogenes  
 XX Sequence 1542 BP; 389 A; 352 C; 487 G; 314 T; 0 U; 0 Other;  
 SQ

Query Match 7.9%; Score 121; DB 4; Length 1542;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTCACGGGGCCCGCAC 925
Db 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTCACGGGGCCCGCAC 936
QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCAACGCGAAGAACCTTACCTGTCTTTGACA 985
Db 937 AAGCGGTGGAGCATGTGGTTTAATTCGATCAACGCGAAGAACCTTACCTGTCTTTGACA 996
QY 986 T 986
Db 997 T 997

RESULT 13
AAF23015
ID AAF23015 standard; rRNA; 1542 BP.
XX
AC AAF23015;
XX
DT 20-MAR-2001 (first entry)
XX
XX E. coli 16S rRNA sequence.
XX
XX Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
XX Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
XX Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrhoeae; fungus;
XX Bacterium; ss.
XX
XX Escherichia coli.
XX
XX US6150517-A.
XX
XX 21-NOV-2000.
XX
XX 30-MAY-1995; 95US-00454063.
XX
XX 24-NOV-1986; 86US-00934244.
XX
XX 07-AUG-1987; 87US-00083542.
XX
XX 24-NOV-1987; 87WO-US003009.
XX
XX 09-DEC-1988; 88US-00295208.
XX
XX 11-DEC-1991; 91US-00806929.
XX
XX 22-FEB-1994; 94US-00200866.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Mcdonough SH, Kop JA, Smith RD, Hogan JJ;
XX
XX WPI; 2001-060029/07.
XX
XX Preparing a probe for nucleic acid hybridization assays comprises
XX constructing a nucleotide polymer sufficiently complementary to hybridize
XX to an rRNA region that distinguishes non-viral target from non-viral non-
XX target species.
XX
XX Disclosure; Fig 1; 75pp; English.
XX
XX The present invention provides novel methods of producing probes for use
XX in the identification of a number of microorganisms. These include E.
XX coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
XX Legionella, Salmonella, Pseudomonas, Neisseria gonorrhoeae, fungi and
XX bacteria
XX
XX Sequence 1542 BP; 389 A; 351 C; 488 G; 0 T; 314 U; 0 Other;
XX
XX Query Match 7.9%; Score 121; DB 5; Length 1542;
XX Best Local Similarity 80.2%; Pred. No. 1.8e-52;
XX Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTCACGGGGCCCGCAC 925
Db 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAATGATTCACGGGGCCCGCAC 936
QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATCAACGCGAAGAACCTTACCTGTCTTTGACA 985
Db 937 AAGCGGTGGAGCATGTGGTTTAATTCGATCAACGCGAAGAACCTTACCTGTCTTTGACA 996
QY 986 T 986
Db 997 T 997

RESULT 14
AAH75410
ID AAH75410 standard; rRNA; 1542 BP.
XX
AC AAH75410;
XX
DT 18-OCT-2001 (first entry)
XX
XX E. coli 16S rRNA.
XX
XX 16S rRNA; 23S rRNA; RNA binding; antimicrobial; ss.
XX
XX Escherichia coli.
XX
XX Key Location/Qualifiers
XX misc_binding 9..13
XX /tag= a
XX /bound moiety= "16S rRNA"
XX /note= "Binds nucleotides 25-21 to form a duplex"
XX
XX misc_binding 17..19
XX /tag= b
XX /bound moiety= "16S rRNA"
XX /note= "Binds nucleotides 918-916 to form a duplex"
XX
XX misc_binding 21..25
XX /tag= c
XX /bound moiety= "16S rRNA"
XX /note= "Binds nucleotides 13-9 to form a duplex"
XX
XX misc_binding 27..37
XX /tag= d
XX /bound moiety= "16S rRNA"
XX /note= "Binds nucleotides 556-547 to form a duplex"
XX
XX misc_binding 39..46
XX /tag= e
XX /bound moiety= "16S rRNA"
XX /note= "Binds nucleotides 403-394 to form a duplex"
XX
XX misc_binding 52..58
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XX /note= "Binds nucleotides 238-221 to form a duplex"
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XX stem_loop 144..178
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XX misc_binding 312..314
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FT 354. .359  
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FT /note= "Binds nucleotides 58-52 to form a duplex"  
FT 367. .392  
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FT 394. .403  
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FT /note= "Binds nucleotides 46-39 to form a duplex"  
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FT 442. .492  
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FT 500. .545  
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FT 547. .556  
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FT /note= "Binds nucleotides 883-881 to form a duplex"  
FT 577. .586  
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FT 725. .732  
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FT 946. .955  
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FT /note= "Binds nucleotides 1044-1037 to form a duplex"  
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~ Best Local Similarity 80.2%; Pred. No. 1.8e-52;

Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGGAGTACGGCGCAAGTTAAACTCAATCAATGACGGGGCCCGCAC 925

Db 877 GACCGCTGGGGAGTACGGCGCAAGTTAAACTCAATCAATGACGGGGCCCGCAC 936



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FT /note= "Binds nucleotides 1210-1192 to form a duplex"
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FT /note= "Binds nucleotides 1073-1068 to form a duplex"
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Query Match 7.9%; Score 121; DB 6; Length 1542;  
Best Local Similarity 80.2%; Pred. No. 1.8e-52;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

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Db 937 AAGCGGUGGAGCAUGUGGUUUAUUCGAUGCAACGCCGAAGAACCUUACCGGUCUUGACA 996
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Db 997 U 997
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GenCore version 5.1.6  
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Gapop 60.0, Gapext 60.0

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	8.9	1485	1 US-08-299-810A-27	Sequence 27, Appl
2	136	8.9	269223	4 US-09-596-002-41	Sequence 41, Appl
3	121	7.9	881	5 PCT-US91-01574-13	Sequence 13, Appl
4	121	7.9	882	2 US-07-923-871C-13	Sequence 13, Appl
5	121	7.9	1487	4 US-09-726-774-14	Sequence 14, Appl
6	121	7.9	1542	1 US-08-114-695A-1	Sequence 1, Appl
7	121	7.9	1542	2 US-08-757-653-158	Sequence 158, App
8	121	7.9	1542	3 US-09-465-355-2	Sequence 2, Appl
9	121	7.9	1542	4 US-08-520-946-158	Sequence 158, App
10	121	7.9	1542	4 US-09-655-378A-158	Sequence 158, App
11	121	7.9	1542	4 US-09-548-998E-33	Sequence 33, Appl
12	121	7.9	1549	4 US-09-492-709A-89	Sequence 89, Appl
13	121	7.9	1549	4 US-09-492-709A-242	Sequence 242, App
14	121	7.9	1549	4 US-09-492-709A-402	Sequence 402, App
15	114	7.5	1541	4 US-09-726-774-2	Sequence 2, Appl
16	110	7.2	1830121	4 US-09-557-884-1	Sequence 1, Appl
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18	110	7.2	1830121	4 US-09-643-990A-1	Sequence 1, Appl
19	110	7.2	1830121	4 US-09-643-990A-1	Sequence 1, Appl
20	109	7.1	1506	4 US-10-278-942-1	Sequence 1, Appl
21	97	6.4	140	2 US-08-744-490-8	Sequence 8, Appl
22	97	6.4	140	2 US-08-744-490-10	Sequence 10, Appl
23	97	6.4	140	2 US-08-744-490-11	Sequence 11, Appl
24	97	6.4	140	2 US-08-744-490-12	Sequence 12, Appl
25	97	6.4	140	2 US-08-744-490-13	Sequence 13, Appl
26	97	6.4	140	2 US-08-744-490-14	Sequence 14, Appl
27	88	5.8	1501	4 US-09-793-920A-1	Sequence 1, Appl

28	88	5.8	1501	4 US-09-821-016-5	Sequence 5, Appl
29	88	5.8	1501	4 US-09-745-476-1	Sequence 1, Appl
30	88	5.8	1501	4 US-09-748-205-1	Sequence 1, Appl
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35	84	5.5	1429	4 US-09-934-868-81	Sequence 81, Appl
36	83	5.4	1449	3 US-09-602-417-1	Sequence 1, Appl
37	83	5.4	1451	3 US-09-342-579-1	Sequence 1, Appl
38	83	5.4	1451	3 US-03-617-854A-1	Sequence 1, Appl
39	83	5.4	1474	1 US-08-114-695A-8	Sequence 8, Appl
40	83	5.4	1495	3 US-09-063-898-1	Sequence 1, Appl
41	83	5.4	1495	4 US-09-985-846-1	Sequence 1, Appl
42	83	5.4	1500	4 US-09-726-774-4	Sequence 4, Appl
43	78	5.1	354	4 US-09-328-352-1462	Sequence 1462, Ap
44	77	5.0	1540	3 US-09-228-184-1	Sequence 1, Appl
45	77	5.0	1540	4 US-09-967-376-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-299-810A-27  
; Sequence 27, Application US/08299810A  
; Patent No. 5721097  
; GENERAL INFORMATION:  
; APPLICANT: Rossau, Rudi  
; APPLICANT: Van Heuverswyn, Hugo  
; TITLE OF INVENTION: HYBRIDIZATION PROBES FOR THE  
; TITLE OF INVENTION: DETECTION OF BRANHAMELLA CATARRHALIS STRAINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5721097west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,810A  
; FILING DATE: 01-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hillson, Randall A.  
; REGISTRATION NUMBER: 31,838  
; REFERENCE/DOCKET NUMBER: 8076.70-US-WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1485 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Branhamella catarrhalis  
; IMMEDIATE SOURCE:  
; CLONE: 16S rRNA Gene  
US-08-299-810A-27

Query Match 8.9%; Score 136; DB 1; Length 1485;  
Best Local Similarity 100.0%; Pred. No. 5.9e-61;  
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RESULT 2
US-09-596-002-41/c
; Sequence 41, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596.002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 269223
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 41
; PUBLICATION INFORMATION:
US-09-596-002-41

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Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 92016 ACCTGGTCTTGACATA 92001

RESULT 3
PCT-US91-01574-13
; Sequence 13, Application PC/TUS9101574
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-Third Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

Qy 852 TAACGCAATAGTAGACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAATGAATTG 911
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Db 929 ACCTGGTCTTGACATA 944

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PCT/US91/01574
APPLICATION NUMBER: PCT/US91/01574
FILING DATE: 19910307
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 489,676
FILING DATE: 07-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kaster, Kevin R.
REGISTRATION NUMBER: 32,704
REFERENCE/DOCKET NUMBER: 2536.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 420-3444
TELEFAX: (415) 658-5239
TELEX: 4992659
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US91-01574-13

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Best Local Similarity 100.0%; Pred. No. 4.5e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 276 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 335
Qy 986 T 986
Db 336 T 336

RESULT 4
US-07-923-871C-13
; Sequence 13, Application US/07923871C
; Patent No. 5912117
; GENERAL INFORMATION:
; APPLICANT: White Ph.D, Thomas J.
; APPLICANT: Dodge, Deborah E.
; TITLE OF INVENTION: Method for Diagnosis of Lyme Disease
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,871C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 489,676
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FILING DATE: 07-MAR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8697  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 892 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-923-871C-13

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Best Local Similarity 100.0%; Pred. No. 4.5e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 276 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTGCTTGTGACA 335  
QY 986 T 986  
DB 336 T 336

RESULT 5  
US-09-726-774-14  
Sequence 14, Application US/09726774  
Patent No. 6677153  
GENERAL INFORMATION:  
APPLICANT: Iversen, Patrick L.  
TITLE OF INVENTION: Antisense Antibacterial Method and  
FILE REFERENCE: 0450-0032.30  
CURRENT APPLICATION NUMBER: US/09/726,774  
CURRENT FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: US 60/168,150  
PRIOR FILING DATE: 1999-11-29  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 1487  
TYPE: DNA  
ORGANISM: Shigella dysenterae  
US-09-726-774-14

Query Match 7.9%; Score 121; DB 4; Length 1487;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAAATGACGGGGCCCGCAC 925  
DB 857 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAAATGACGGGGCCCGCAC 916  
QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTGCTTGTGACA 985  
DB 917 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTGCTTGTGACA 976  
QY 986 T 986  
DB 977 T 977

## RESULT 6

US-08-114-695A-1  
Sequence 1, Application US/08114695A  
Patent No. 5508193  
GENERAL INFORMATION:  
APPLICANT: Mandelbaum, Raphael T.  
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND  
TITLE OF INVENTION: WATER  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.  
STREET: 3500 IDS CENTER  
CITY: MINNEAPOLIS  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/114,695A  
FILING DATE: 31-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MUETING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 600.268US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3081  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: rRNA  
ORIGINAL SOURCE:  
ORGANISM: Escherichia coli  
US-08-114-695A-1

Query Match 7.9%; Score 121; DB 1; Length 1542;  
Best Local Similarity 80.2%; Pred. No. 4.4e-53;  
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAAATGACGGGGCCCGCAC 925  
DB 877 GACCGCTGGGAGTACGCGCGCAAGGTTAAACTCAAAATGAAATGACGGGGCCCGCAC 936  
QY 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTGCTTGTGACA 985  
DB 937 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGCGAAGAACCTTACTGCTTGTGACA 996  
QY 986 T 986  
DB 997 U 997

## RESULT 7

US-08-757-653-158  
Sequence 158, Application US/08757653  
Patent No. 5843669  
GENERAL INFORMATION:  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Lyamichev, Natasha  
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

```

; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-653-158

Query Match 7.9%; Score 121; DB 2; Length 1542;
Best Local Similarity 100.0%; Pred. No. 4.4e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATGACGGGGCCGCGAC 925
DB 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATGACGGGGCCGCGAC 936
QY 926 AAGCGGTGACATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985
DB 937 AAGCGGTGACATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 996
QY 986 T 986
DB 997 T 997

RESULT 8
US-09-465-355-2
; Sequence 2, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05

; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1542
; TYPE: RNA
; ORGANISM: Escherichia coli
US-09-465-355-2

Query Match 7.9%; Score 121; DB 3; Length 1542;
Best Local Similarity 80.2%; Pred. No. 4.4e-53;
Matches 97; Conservative 24; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATGACGGGGCCGCGAC 925
DB 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATGACGGGGCCGCGAC 936
QY 926 AAGCGGTGACATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 985
DB 937 AAGCGGTGACATGTGTTTAAATTCGATGCAACGCGAAGACCTTACCTGGTCTTGACA 996
QY 986 T 986
DB 997 U 997

RESULT 9
US-08-520-946-158
; Sequence 158, Application US/08520946
; Patent No. 6372424
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; APPLICANT: LYAMICHEV, VICTOR I.
; APPLICANT: OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,946
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-946-158

Query Match 7.9%; Score 121; DB 3; Length 1542;
Best Local Similarity 100.0%; Pred. No. 4.4e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAAATGAATGACGGGGCCGCGAC 925
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Db 877 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 10

US-09-655-378A-158  
; Sequence 158, Application US/09655378A  
; Patent No. 6673616  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; LYAMICHEV, VICTOR I.  
; OLIVE, DAVID M.  
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
; PATHOGENS

; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/655,378A  
; FILING DATE: 05-Sep-2000  
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 158:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1542 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (Genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 158:

US-09-655-378A-158  
Query Match 7.9%; Score 121; DB 4; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 925  
Db 877 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 11

US-09-548-998E-33  
; Sequence 33, Application US/09548998E  
; Patent No. 6797817  
; GENERAL INFORMATION:  
; APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY, INC.  
; APPLICANT: EBERSOLE, RICHARD C.  
; APPLICANT: HENDRICKSON, EDWIN  
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING B  
; FILE REFERENCE: BC1002 US NA  
; CURRENT APPLICATION NUMBER: US/09/548,998E  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/129,511  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 1542  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; US-09-548-998E-33

Query Match 7.9%; Score 121; DB 4; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 925  
Db 877 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 936  
Qy 926 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 985  
Db 937 AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACCGGAAGAACCTTACCTGCTCTTGACA 996  
Qy 986 T 986  
Db 997 T 997

RESULT 12

US-09-492-709A-89  
; Sequence 89, Application US/09492709A  
; Patent No. 6720139  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001A  
; CURRENT APPLICATION NUMBER: US/09/492,709A  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
; US-09-492-709A-89

Query Match 7.9%; Score 121; DB 4; Length 1549;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 925  
Db 878 GACCGCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATGACGGGGCCCGCAC 937

Qy	926	AAGCGTGGAGCATCTGCTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA	985
Db	938	AAGCGTGGAGCATCTGCTTTAATTCGATCGAACGCGAAGAACCTTACCTGGTCTTGACA	997
Qy	986	T	986
		—	
Db	998	T	998

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RESULT 13
US-09-492-709A-242
; Sequence 242, Application US/09492709A
; Patent No. 6720139
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Froelich, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; TITLE OF INVENTION: ESCHERICHIA COLI
; FILE REFERENCE: ELITRA 001A
; CURRENT APPLICATION NUMBER: US/09/492,709A
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 242
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: E. Coli
US-09-492-709A-242

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	Query Match	7.9%;	Score 121;	DB 4;	Length 1549;
	Best Local Similarity	100.0%;	Pred. No. 4.4e-53;		
	Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	866	GACGCGCTGGGGAGTACGGCCGAAGGTTAAACTCAAATGAAATGACGGGGCCCGCAC	925		
Db	878	GACGCGCTGGGGAGTACGGCCGAAGGTTAAACTCAAATGAAATGACGGGGCCCGCAC	937		
Qy	926	AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGGGAACCTTACCTGCTTTGACA	985		
Db	938	AAGCGGTGGAGCATGTGTTTAAATTCGATGCAACGGGAACCTTACCTGCTTTGACA	997		
Qy	986	T	986		
Db	998	T	998		

RESULT 14  
US-09-492-709A-402  
; Sequence 402, Application US/09492709A  
; Patent No. 6720139  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; TITLE OF INVENTION: ESCHERICHIA COLI  
; FILE REFERENCE: ELITRA.001A  
; CURRENT APPLICATION NUMBER: US/09/492,709A  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 402

Search completed: April 12, 2005, 14:29:39  
Job time : 286 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 12:56:39 ; Search time 940 Seconds  
(without alignments)  
9837.835 Million cell updates/sec

Title: US-09-979-558A-1  
Perfect score: 1526  
Sequence: 1 ttgatcatggctccagatt.....acctgcggtgatcacctc 1526

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 5615251 seqs, 3030001701 residues

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Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
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22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	136	8.9	269223	17 US-10-672-787-41	Sequence 41, Appl
2	121	7.9	549	10 US-09-991-936-1717	Sequence 1717, Ap
3	121	7.9	1487	9 US-09-726-774-14	Sequence 14, Appl
4	121	7.9	1487	18 US-10-719-633-14	Sequence 14, Appl
5	121	7.9	1505	9 US-09-027-439-6	Sequence 6, Appl
6	121	7.9	1506	9 US-09-027-439-3	Sequence 3, Appl
7	121	7.9	1534	16 US-10-029-397A-35	Sequence 35, Appl
8	121	7.9	1541	9 US-09-027-439-7	Sequence 7, Appl
9	121	7.9	1542	10 US-09-940-925A-158	Sequence 158, App
10	121	7.9	1542	10 US-09-941-193A-158	Sequence 158, App
11	121	7.9	1542	14 US-10-061-071-33	Sequence 33, Appl

12	121	7.9	1549	9 US-09-912-020-89	Sequence 89, Appl
13	121	7.9	1549	9 US-09-912-020-242	Sequence 242, App
14	121	7.9	1549	9 US-09-912-020-402	Sequence 402, App
15	121	7.9	1549	18 US-10-771-241-89	Sequence 89, Appl
16	121	7.9	1549	18 US-10-771-241-242	Sequence 242, App
17	121	7.9	1549	18 US-10-771-241-402	Sequence 402, App
c 18	121	7.9	10903	18 US-10-612-224-1	Sequence 1, Appl
c 19	121	7.9	11918	18 US-10-612-224-2	Sequence 2, Appl
20	121	7.9	13278	18 US-10-612-224-3	Sequence 3, Appl
21	116	7.6	1494	13 US-10-007-725-5	Sequence 5, Appl
22	114	7.5	1541	9 US-09-726-774-2	Sequence 2, Appl
23	114	7.5	1541	18 US-10-719-633-2	Sequence 2, Appl
24	112	7.3	1324	18 US-10-808-807-16	Sequence 16, Appl
25	112	7.3	1331	18 US-10-804-677-16	Sequence 16, Appl
26	110	7.2	1327	18 US-10-808-979-16	Sequence 16, Appl
27	110	7.2	1351	19 US-10-810-733-18	Sequence 18, Appl
28	110	7.2	1455	18 US-10-761-509-1	Sequence 1, Appl
29	110	7.2	1485	16 US-10-029-397A-36	Sequence 36, Appl
30	110	7.2	1830121	17 US-10-329-670-1	Sequence 1, Appl
c 31	110	7.2	1830121	17 US-10-329-670-1	Sequence 1, Appl
32	110	7.2	1830121	18 US-10-158-865-1	Sequence 1, Appl
c 33	110	7.2	1830121	18 US-10-158-865-1	Sequence 1, Appl
34	109	7.1	1506	16 US-10-378-942-1	Sequence 1, Appl
35	108	7.1	1486	9 US-09-737-297-1	Sequence 1, Appl
36	101	6.6	1542	18 US-10-361-002-6	Sequence 6, Appl
37	101	6.6	1542	18 US-10-361-004-6	Sequence 6, Appl
38	99	6.5	1453	9 US-09-027-439-5	Sequence 5, Appl
39	95	6.2	1481	9 US-09-737-297-4	Sequence 4, Appl
40	94	6.2	1131	18 US-10-704-751-1	Sequence 1, Appl
41	88	5.8	1070	9 US-09-737-297-2	Sequence 2, Appl
42	88	5.8	1140	9 US-09-737-297-5	Sequence 5, Appl
43	88	5.8	1420	19 US-10-875-006-1	Sequence 1, Appl
44	88	5.8	1424	14 US-10-007-527A-12	Sequence 12, Appl
45	88	5.8	1424	14 US-10-007-452-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-10-672-787-41/c  
; Sequence 41, Application US/10672787  
; Publication No. US200400067554A1  
; GENERAL INFORMATION:  
; APPLICANT: LAGACE, Robert, E.  
; APPLICANT: PATTERSON, Chandra  
; APPLICANT: BERG, Kim, L.  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME  
; FILE REFERENCE: ELITRA.025C1  
; CURRENT APPLICATION NUMBER: US/10/672,787  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 09/596,002  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PERL Program  
; SEQ ID NO 41  
; LENGTH: 269223  
; TYPE: DNA  
; ORGANISM: Moraxella catarrhalis  
US-10-672-787-41

Query Match	8.9%	Score 136;	DB 17;	Length 269223;
Best Local Similarity	100.0%	Pred. No. 9e-62;		
Matches 136;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	852	TAACGCAATAGTAGACCGCTGGGGAGTAGCGCGCAGGTTAAACTCAATGAATTG	911	
Db	92136	TAACGCAATAGTAGACCGCTGGGGAGTAGCGCGCAGGTTAAACTCAATGAATTG	92077	
Qy	912	ACGGGGCCCGCACACGCGTGGAGCATGTGTTTAAATTCGATCAACGCCGAAGACCTT	971	
Db	92076	ACGGGGCCCGCACACGCGTGGAGCATGTGTTTAAATTCGATCAACGCCGAAGACCTT	92017	

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QY 972 ACCTGGTCTTGACATA 987
Db 92016 ACCTGGTCTTGACATA 92001

RESULT 2
US-09-991-936-1717
; Sequence 1717, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1717
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-1717

Query Match 7.9%; Score 121; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 925
Db 163 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 222

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 223 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 282

QY 986 T 986
Db 283 T 283

RESULT 3
US-09-726-774-14
; Sequence 14, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenteriae
US-09-726-774-14

Query Match 7.9%; Score 121; DB 9; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 ACCTGGTCTTGACATA 987
Db 92016 ACCTGGTCTTGACATA 92001

RESULT 2
US-09-991-936-1717
; Sequence 1717, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-6-C1
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1717
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-1717

Query Match 7.9%; Score 121; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 925
Db 163 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 222

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 223 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 282

QY 986 T 986
Db 283 T 283

RESULT 3
US-09-726-774-14
; Sequence 14, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenteriae
US-09-726-774-14

Query Match 7.9%; Score 121; DB 9; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 972 ACCTGGTCTTGACATA 987
Db 92016 ACCTGGTCTTGACATA 92001

RESULT 2
US-10-719-633-14
; Sequence 14, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenterae
US-10-719-633-14

Query Match 7.9%; Score 121; DB 18; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 925
Db 857 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 916

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 917 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 976

QY 986 T 986
Db 977 T 977

RESULT 4
US-10-719-633-14
; Sequence 14, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Shigella dysenterae
US-10-719-633-14

Query Match 7.9%; Score 121; DB 18; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.3e-53;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 925
Db 857 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATTTGACGGGGGCCGCGAC 916

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 917 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 976

QY 986 T 986
Db 977 T 977

RESULT 5
US-09-027-439-6
; Sequence 6, Application US/09027439A
; Patent No. US20020006611A1
; GENERAL INFORMATION:
; APPLICANT: Portugal, Frank H.
; APPLICANT: Colwell, Rita R.
; APPLICANT: Hug, Anwarul
; APPLICANT: Chowdhury, Afzal
; TITLE OF INVENTION: Compositions and Methods for Differentiating Among
; TITLE OF INVENTION: Shigella Species and Shigella from E. coli Species
; FILE REFERENCE: 044198/0000
; CURRENT APPLICATION NUMBER: US/09/027,439A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/038,117
; EARLIER FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1505

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; TYPE: DNA
; ORGANISM: Shigella boydii
US-09-027-439-6

Query Match
Best Local Similarity 7.9%; Score 121; DB 9; Length 1505;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 925
|
Db 868 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 927
|
QY 926 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 985
|
Db 928 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 987
|
QY 986 T 986
|
Db 988 T 988

RESULT 6
US-09-027-439-3
; Sequence 3, Application US/09027439A
; Patent No. US20020006611A1
; GENERAL INFORMATION:
; APPLICANT: Portugal, Frank H.
; APPLICANT: Colwell, Rita R.
; APPLICANT: Huq, Anwarul
; APPLICANT: Chowdhury, Afzal
; TITLE OF INVENTION: Compositions and Methods for Differentiating Among
; FILE OF INVENTION: Shigella Species and Shigella from E. coli Species
; CURRENT APPLICATION NUMBER: US/09/027,439A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/038,117
; EARLIER FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Shigella flexneri
US-09-027-439-3

Query Match
Best Local Similarity 7.9%; Score 121; DB 9; Length 1506;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 925
|
Db 870 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 929
|
QY 926 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 985
|
Db 930 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 989
|
QY 986 T 986
|
Db 990 T 990

RESULT 7
US-10-029-397A-35
; Sequence 35, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMB1:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
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; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 1534
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (11)..(12)
; OTHER INFORMATION: N = A, C, G or T/U
US-10-029-397A-35

Query Match
Best Local Similarity 7.9%; Score 121; DB 16; Length 1534;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 925
|
Db 869 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 928
|
QY 926 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 985
|
Db 929 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 988
|
QY 986 T 986
|
Db 989 T 989

RESULT 8
US-09-027-439-7
; Sequence 7, Application US/09027439A
; Patent No. US20020006611A1
; GENERAL INFORMATION:
; APPLICANT: Portugal, Frank H.
; APPLICANT: Colwell, Rita R.
; APPLICANT: Huq, Anwarul
; APPLICANT: Chowdhury, Afzal
; TITLE OF INVENTION: Compositions and Methods for Differentiating Among
; FILE OF INVENTION: Shigella Species and Shigella from E. coli Species
; CURRENT APPLICATION NUMBER: US/09/027,439A
; CURRENT FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/038,117
; EARLIER FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-027-439-7

Query Match
Best Local Similarity 7.9%; Score 121; DB 9; Length 1541;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 925
|
Db 876 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAAATGAATTTGACGGGGGGCCGCAC 935
|
QY 926 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 985
|
Db 936 AAGCGGTGAGCATGTGGTTAAATTCGATGCAACCGAAGAACCTTACTGCTTTTGACA 995
|
QY 986 T 986
|
Db 996 T 996

RESULT 9
US-09-940-925A-158
; Sequence 158, Application US/09940925A
```

Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 158:  
US-09-940-925A-158  
Query Match 7.9%; Score 121; DB 10; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATGACGGGGCCCCGCAC 925  
DB 877 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATGACGGGGCCCCGCAC 936  
QY 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
DB 937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 996  
QY 986 T 986  
DB 997 T 997  
RESULT 10  
US-09-941-193A-158  
Sequence 158, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 158:  
US-09-941-193A-158  
Query Match 7.9%; Score 121; DB 10; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 866 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATGACGGGGCCCCGCAC 925  
DB 877 GACCGCTGGGAGTAGCGCGCAAGGTTAAACTCAAATGAATGACGGGGCCCCGCAC 936  
QY 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
DB 937 AAGCGGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 996  
QY 986 T 986  
DB 997 T 997  
RESULT 11  
US-10-061-071-33  
Sequence 33, Application US/10061071  
Publication No. US20030077601A1  
GENERAL INFORMATION:  
APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY  
APPLICANT: HENDRICKSON, EDWIN  
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING  
BACTERIA  
FILE REFERENCE: BC1002 US CIP  
CURRENT APPLICATION NUMBER: US/10/061,071  
CURRENT FILING DATE: 2002-01-29  
PRIOR APPLICATION NUMBER: US 60/129,511  
PRIOR FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: 60/129,511  
PRIOR FILING DATE: 1999-04-15  
NUMBER OF SEQ ID NOS: 103  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 33  
TYPE: DNA  
LENGTH: 1542  
ORGANISM: Escherichia coli  
US-10-061-071-33  
Query Match 7.9%; Score 121; DB 14; Length 1542;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 925  
|  
Db 877 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 936  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
|  
Db 937 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 996  
|  
Qy 986 T 986  
|  
Db 997 T 997

## RESULT 12

US-09-912-020-89  
; Sequence 89, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
US-09-912-020-89

Query Match 7.9%; Score 121; DB 9; Length 1549;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 866 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 925  
|  
Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 937  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
|  
Db 938 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 997  
|  
Qy 986 T 986  
|  
Db 998 T 998

## RESULT 13

US-09-912-020-242  
; Sequence 242, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 242  
; LENGTH: 1549  
; TYPE: DNA  
; ORGANISM: E. Coli  
US-09-912-020-242

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Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
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Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 937  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 985  
|  
Db 938 AAGCGTGGAGCATGTGTTTAATTCGATGCAACCGGAAGAACCTTACCTGGTCTTGACA 997  
|  
Qy 986 T 986  
|  
Db 998 T 998

## RESULT 14

US-09-912-020-402  
; Sequence 402, Application US/09912020  
; Patent No. US20020045592A1  
; GENERAL INFORMATION:  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Trawick, John  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Froelich, Jamie M.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN  
; FILE REFERENCE: ELITRA.001DV1  
; CURRENT APPLICATION NUMBER: US/09/912,020  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/492,709  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/117,405  
; PRIOR FILING DATE: 1999-01-27  
; NUMBER OF SEQ ID NOS: 485  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 402  
; LENGTH: 1549  
; TYPE: RNA  
; ORGANISM: E. Coli  
US-09-912-020-402

Query Match 7.9%; Score 121; DB 9; Length 1549;  
Best Local Similarity 80.2%; Pred. No. 1.3e-53;  
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|  
Db 878 GACCGCTGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGCCCGCAC 937  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 10:39:14 ; Search time 5290 Seconds  
(without alignments)  
10980.354 Million cell updates/sec

Title: US-09-979-558A-1  
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Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	121	7.9	247	CB393967	OSTR129G4
2	121	7.9	394	BH819649	BACPP13-M
3	121	7.9	437	BH835798	BACPP9-A0
4	121	7.9	465	BG357866	OV2_31-C0
5	121	7.9	473	BH831257	BACPP33-C
6	121	7.9	522	BH826849	BACPP24-C
7	121	7.9	524	BH822044	BACPP17-A
8	121	7.9	542	CF339295	RCL1--04-
9	121	7.9	592	AG019018	Homo sapi
10	121	7.9	609	BQ152671	NF022A12I
11	121	7.9	639	BH818000	BACPP10-K
12	121	7.9	646	BH822078	BACPP17-E
13	121	7.9	646	BH833826	BACPP5-P0
14	121	7.9	658	CF339842	RCL1--06-
15	121	7.9	661	BH820342	BACPP14-O
16	121	7.9	745	CF566443	1115107G1
17	121	7.9	770	CF557211	1115025D0
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20	103	6.7	516	AG613313	Escherich
21	99	6.5	714	BE202334	SNOWMFCAR
22	94	6.2	383	BE427965	MTD001-1
23	88	5.8	502	AU312474	AU312474
24	88	5.8	676	BE187622	EST336183

25	88	5.8	735	6	CD423027	CD423027
26	88	5.8	1010	8	BZ566539	pacB2-164
27	88	5.8	1068	8	BZ576658	mh2_5045
28	88	5.8	1205	8	BZ566538	pacB2-164
29	88	5.8	1507	8	BZ576476	mh2_4950
30	86	5.6	184	2	AW834377	MR2-TT001
31	86	5.6	503	6	CD423957	SA1_2_B04
32	86	5.6	516	4	BM335455	MEST162-A
33	86	5.6	521	4	BM332487	MEST169-P
34	86	5.6	527	4	BM348070	MEST286-B
35	86	5.6	559	2	BF845685	780B5 CDN
36	86	5.6	569	1	A1779239	EST260118
37	86	5.6	604	2	BE204135	EST396811
38	86	5.6	660	2	AW600903	3B5 CDNA
39	86	5.6	851	7	CK290947	CK390947
40	86	5.6	884	7	CK280528	EST753661
41	86	5.6	889	7	CK280527	EST743249
42	86	5.6	941	7	CK296497	EST759211
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ALIGNMENTS

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LOCUS OSTR129G4\_1 AD-wrmcDNA Caenorhabditis elegans cdna, mRNA linear EST 15-MAY-2003  
DEFINITION CB393967  
ACCESSION CB393967  
VERSION CB393967.1 GI:30735678  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans  
ORGANISM Caenorhabditis elegans  
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
1 (bases 1 to 247)  
AUTHORS Rebul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tollas,P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.  
TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression  
JOURNAL Nat. Genet. (2003) In press  
COMMENT Contact: Vidal M  
Marc Vidal Laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david\_hill@dfci.harvard.edu or marc\_vidal@dfci.harvard.edu  
POLYA=No.

FEATURES

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/organism="Caenorhabditis elegans"  
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/sex="Hermaphrodite and male"  
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/clone\_lib="AD-wrmcDNA"  
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subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN
Query Match          7.9%; Score 121; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 925
Db 64 GACCGCTGGGAGTACGGCGCAAGGTTAAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 123
Qy 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 124 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 183
Qy 986 T 986
Db 184 T 184

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LOCUS
DEFINITION BACPP13-M12.y Pristionchus pacificus BAC ends Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION BH819649
VERSION BH819649.1 GI:20993980
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 394)
AUTHORS Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Mollare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
pacificus
JOURNAL Unpublished (2002)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
source
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/clone_lib="Pristionchus pacificus BAC ends"

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Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 283 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 342
Qy 986 T 986
Db 343 T 343

RESULT 3
BH835798
LOCUS
DEFINITION BACPP9-A07.z Pristionchus pacificus BAC ends Pristionchus pacificus
genomic, genomic survey sequence.
ACCESSION BH835798
VERSION BH835798.1 GI:21038085
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 437)
AUTHORS Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Mollare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
pacificus
JOURNAL Unpublished (2002)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
source
1. .437
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Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985
Db 280 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 339
Qy 986 T 986
Db 340 T 340

RESULT 4
BG357866
LOCUS
DEFINITION OV2_31_C04.bl_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BG357866
VERSION BG357866.1 GI:13239852
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 465)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
An EST database from Sorghum: ovaries of varying immature stages
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM

```

Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Seq primer: JEN REV  
High quality sequence stop: 463  
POLYA=No.

#### FEATURES

Location/Qualifiers

1..465  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
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/clone\_lib="Ovary 2 (OV2)"  
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#### ORIGIN

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198 GACCGCTGGGAGTACGGCCGCAAGTTAAACTCAAATGAATGACGGGGCCCGCAC 257  
|  
Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 985  
Db |  
258 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 317  
|  
Qy 986 T 986  
Db 318 T 318

#### RESULT 5

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DEFINITION BACPP33-C16.Y Pristionchus pacificus BAC ends Pristionchus  
pacificus genomic, genomic survey sequence.  
ACCESSION BH831257  
VERSION BH831257.1 GI:21028759  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

#### REFERENCE

AUTHORS Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,  
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,  
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.  
TITLE A BAC-based genetic linkage map of the nematode Pristionchus  
pacificus  
JOURNAL Unpublished (2002)  
COMMENT Contact: Sommer RJ

#### ORIGIN

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.  
Location/Qualifiers

#### FEATURES

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#### ORIGIN

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Db |  
223 GACCGCTGGGAGTACGGCCGCAAGTTAAACTCAAATGAATGACGGGGCCCGCAC 282  
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Qy 926 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 985  
Db |  
283 AAGCGTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGCTTTGACA 342  
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Qy 986 T 986  
Db 343 T 343

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pacificus genomic, genomic survey sequence.  
ACCESSION BH826849  
VERSION BH826849.1 GI:21019674  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

#### REFERENCE

AUTHORS Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,  
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,  
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.  
TITLE A BAC-based genetic linkage map of the nematode Pristionchus  
pacificus  
JOURNAL Unpublished (2002)  
COMMENT Contact: Sommer RJ

#### ORIGIN

Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends  
Location/Qualifiers

#### FEATURES

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#### ORIGIN

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Db |  
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Qy 986 T 986  
Db 340 T 340

#### RESULT 7

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LOCUS          BACP17-A15.y Pristionchus pacificus BAC ends Pristionchus
DEFINITION     pacificus genomic, genomic survey sequence.
ACCESSION      BH822044
VERSION        BH822044.1 GI:20998383
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
               Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
               Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 524)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
               Raddatz,G., Witter,H., Keller,H., Kipping,I., Pires da Silva,A.,
               Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
               pacificus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
               Evolutionary Biology
               Max-Planck-Institute for Developmental Biology
               Spemannstr. 37-39, Tuebingen D-72076, Germany
               Tel: 00497071601371
               Fax: 00497071601498
               Email: ralf.sommer@tuebingen.mpg.de
               Class: BAC ends.
               Location/Qualifiers
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QY 926 AAGCGGTGGAGCATGTGTTTAATTCGATCGACGCGAAGACCTTACCTGGTCTTGACA 985
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DB 283 AAGCGGTGGAGCATGTGTTTAATTCGATCGACGCGAAGACCTTACCTGGTCTTGACA 342
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QY 986 T 986
      |
DB 343 T 343

RESULT 8
CF339295
LOCUS          CF339295      542 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION     RCL1--04-G22.g1 Regenerated callus lambda phage cDNA library (RCL1)
               Oryza sativa (japonica cultivar-group) cDNA clone RCL1--04-G22,
               mRNA sequence.
ACCESSION      CF339295
VERSION        CF339295.1 GI:33826975
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 542)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..542
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="RCL1--04-G22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SstI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with SstI and 3' end with XhoI site. Callus was
induced on 2N6 media for 30 days and cultured for 36hrs on
regenerated media"
ORIGIN
Query Match      7.9%; Score 121; DB 7; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCCGCAC 925
      |||||
DB 259 GACCGCTGGGGAGTACGGCGCAAGGTTAAACTCAATGAATGACGGGGGCCGCAC 318
      |||||

QY 926 AAGCGGTGGAGCATGTGTTTAATTCGATCGACGCGAAGACCTTACCTGGTCTTGACA 985
      |||||
DB 319 AAGCGGTGGAGCATGTGTTTAATTCGATCGACGCGAAGACCTTACCTGGTCTTGACA 378
      |||||

QY 986 T 986
      |
DB 379 T 379

RESULT 9
AG019018
LOCUS          AG019018      592 bp      DNA      linear      GSS 09-JAN-2003
DEFINITION     Homo sapiens genomic DNA, 21q region, clone: B753B2BB067R, genomic
               survey sequence.
ACCESSION      AG019018
VERSION        AG019018.1 GI:6017504
KEYWORDS       GSS.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
               Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
TITLE          Homo sapiens genomic DNA, chromosome 21q
JOURNAL        Published Only in Database (1999)
REFERENCE      2 (bases 1 to 592)
AUTHORS        Hattori,M., Fujiyama,A., Ishii,K., Toyoda,A., Taylor,T.,
               Park,H.-S., Yada,T., Watanabe,H. and Sakaki,Y.
TITLE          Direct Submission
JOURNAL        Submitted (10-OCT-1999) Masahira Hattori, RIKEN Genomic Sciences
               Center(GSC) c/o Kitasato University; 1-15-1 Kitasato, Sagami-hara,
               Kanagawa 228-8555, Japan (E-mail:hattori@gsc.ims.u-cokyo.ac.jp,
               Tel:81-42-778-9923, Fax:81-42-778-9924)
               Location/Qualifiers
FEATURES       1..592
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /chromosome="21"
               /map="21q"

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/clone="B753B2B067R"

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ORIGIN
Query Match          7.9%; Score 121; DB 9; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 925
      |||||
Db 174 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 233

Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 985
      |||||
Db 234 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 293

Qy 986 T 986
      |
Db 294 T 294

RESULT 10
B0152671
LOCUS B0152671 609 bp mRNA linear EST 24-APR-2002
DEFINITION NF022A12IR1097 Irradiated Medicago truncatula cDNA clone
          NF022A12IR 5', mRNA sequence.
ACCESSION B0152671
VERSION B0152671.1 GI:20289730
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
          Medicago.
REFERENCE 1 (bases 1 to 609)
          Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
          Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
          Expressed Sequence Tags from the Samuel Roberts Noble Foundation
          Medicago truncatula irradiated library
          Unpublished (2001)
          Contact: May GD
          Plant Biology Division
          The Samuel Roberts Noble Foundation
          2510 Sam Noble Parkway, Ardmore, OK 73402, USA
          Tel: 580 224 6650
          Fax: 580 224 6692
          Email: gdmay@noble.org
Insert Length: 609 Std Error: 0.00
Plate: 022 row: A column: 12
Seq primer: TCACACAGGAACAGCTATGAC.
          Location/Qualifiers
            1..609
              /organism="Medicago truncatula"
              /mol_type="mRNA"
              /db_xref="taxon:3880"
              /clone="NF022A12IR"
              /tissue_type="seedlings"
              /dev_stage="seedling"
              /clone_lib="irradiated"
              /note="Vector: Lambda Zap; Seedlings were exposed either
              to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
              Gamma-irradiated samples were harvested at 6, 12, 24 and
              48 hours after treatment. UV-irradiated samples were
              harvested 24 hours post-treatment. cDNA was prepared from
              polyA+ enriched, pooled samples of equivalent amounts of
              total RNA from each sample. The cDNA was directionally
              ligated into the Uni-Zap XR vector (Stratagene) and
              packaged using the Gigapack III Gold packaging extracts.
              Phagemids containing cDNA inserts were in vivo excised
              from the recombinant Uni-Zap XR vector using EXAssist
              helper phage and the E. coli strain XL1-Blue MRF'
              (Stratagene). Excised plasmids were plated using SOLR
              cells."
FEATURES
source

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ORIGIN

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Query Match          7.9%; Score 121; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 925
      |||||
Db 368 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 427

Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 985
      |||||
Db 428 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 487

Qy 986 T 986
      |
Db 488 T 488

RESULT 11
B018000
LOCUS B018000 639 bp DNA linear GSS 20-MAY-2002
DEFINITION BACPP10-K24.y Pristionchus pacificus BAC ends Pristionchus
          pacificus genomic, genomic survey sequence.
ACCESSION B018000
VERSION B018000.1 GI:20989984
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
          Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
          Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 639)
          Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
          Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
          Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
          A BAC-based genetic linkage map of the nematode Pristionchus
          pacificus
          Unpublished (2002)
          Contact: Sommer RJ
          Evolutionary Biology
          Max-Planck-Institute for Developmental Biology
          Spemannstr. 37-39, Tuebingen D-72076, Germany
          Tel: 00497071601371
          Fax: 00497071601498
          Email: ralf.sommer@tuebingen.mpg.de
          Class: BAC ends.
          Location/Qualifiers
            1..639
              /organism="Pristionchus pacificus"
              /mol_type="genomic DNA"
              /strain="var. California"
              /db_xref="taxon:54126"
              /clone_lib="Pristionchus pacificus BAC ends"
FEATURES
source

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ORIGIN

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Query Match          7.9%; Score 121; DB 8; Length 639;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 925
      |||||
Db 220 GACCCCTGGGGAGTACGGCCGCAAGGTTAAACTCAAATGAATGACGGGGGCGCGCAC 279

Qy 926 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 985
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Db 280 AAGCGGTGGAGCATGTGTTTAATTCGATGCACCGGAAGACCTTACTGCTTTGACA 339

Qy 986 T 986
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Db 340 T 340

RESULT 12

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BH822078      BH822078      646 bp      DNA      linear      GSS 20-MAY-2002
LOCUS          BACPPI7-E05.y Pristionchus pacificus BAC ends Pristionchus
DEFINITION     pacificus genomic, genomic survey sequence.
ACCESSION      BH822078
VERSION        BH822078.1 GI:20998480
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 646)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES             Location/Qualifiers
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                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="var. California"
                     /db_xref="taxon:54126"
                     /clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match      7.9%; Score 121; DB 8; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      866  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTCACGGGGCCGCAC 925
Db      223  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTCACGGGGCCGCAC 282
Qy      926  AAGCGGTGGAGCATGTGTTTAAATTCGATCGCAACGCGAAGACCTTACCTGGTCTTGACA 985
Db      283  AAGCGGTGGAGCATGTGTTTAAATTCGATCGCAACGCGAAGACCTTACCTGGTCTTGACA 342
Qy      986  T 986
Db      343  T 343

RESULT 14
CF339842
LOCUS          CF339842      658 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION     RCL1--06-B12.g1 Regenerated callus lambda phage cDNA library (RCL1)
                Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-B12,
                mRNA sequence.
ACCESSION      CF339842.1 GI:33828055
VERSION        CF339842
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 658)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="RCL1--06-B12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
                     (RCL1)"
                     /notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                     end with SstI and 3' end with XhoI site. Callus was

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BH822078      BH822078      646 bp      DNA      linear      GSS 20-MAY-2002
LOCUS          BACPPI7-E05.y Pristionchus pacificus BAC ends Pristionchus
DEFINITION     pacificus genomic, genomic survey sequence.
ACCESSION      BH822078
VERSION        BH822078.1 GI:20998480
KEYWORDS       GSS.
SOURCE         Pristionchus pacificus
ORGANISM       Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE      1 (bases 1 to 646)
AUTHORS        Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
TITLE          A BAC-based genetic linkage map of the nematode Pristionchus
JOURNAL        Unpublished (2002)
COMMENT        Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES             Location/Qualifiers
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                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:54126"
                     /clone_lib="Pristionchus pacificus BAC ends"

ORIGIN
Query Match      7.9%; Score 121; DB 8; Length 646;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      866  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTCACGGGGCCGCAC 925
Db      223  GACCGCTGGGAGTACGGCGCAAGGTTAAACTCAATGAATTCACGGGGCCGCAC 282
Qy      926  AAGCGGTGGAGCATGTGTTTAAATTCGATCGCAACGCGAAGACCTTACCTGGTCTTGACA 985
Db      283  AAGCGGTGGAGCATGTGTTTAAATTCGATCGCAACGCGAAGACCTTACCTGGTCTTGACA 342
Qy      986  T 986
Db      343  T 343

RESULT 14
CF339842
LOCUS          CF339842      658 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION     RCL1--06-B12.g1 Regenerated callus lambda phage cDNA library (RCL1)
                Oryza sativa (japonica cultivar-group) cDNA clone RCL1--06-B12,
                mRNA sequence.
ACCESSION      CF339842.1 GI:33828055
VERSION        CF339842
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 658)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..658
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="RCL1--06-B12"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
                     (RCL1)"
                     /notes="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                     end with SstI and 3' end with XhoI site. Callus was

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induced on 2N6 media for 30 days and cultured for 36hrs on  
regenerated media"

Search completed: April 12, 2005, 14:24:54  
Job time : 5298 secs

## ORIGIN

Query Match 7.9%; Score 121; DB 7; Length 658;  
Best Local Similarity 100.0%; Pred. No. 2.4e-56;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAATGAATTAACGGGGGCCCGCAC 925  
|||||  
Db 258 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAATGAATTAACGGGGGCCCGCAC 317  
|||||

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
|||||  
Db 318 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 377  
|||||

QY 986 T 986  
378 T 378

## RESULT 15

BH820342  
LOCUS BH820342 661 bp DNA linear GSS 20-MAY-2002  
DEFINITION BACP14-004.y Pristionchus pacificus BAC ends Pristionchus  
pacificus genomic, genomic survey sequence.

## ACCESSION

BH820342

## VERSION

BH820342.1

## KEYWORDS

GSS.

## SOURCE

Pristionchus pacificus

## ORGANISM

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 661)

Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R.,

Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A.,

Jesse, T., Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J.

A BAC-based genetic linkage map of the nematode Pristionchus

pacificus

Unpublished (2002)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

Location/Qualifiers

1..661

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="var. California"

/db\_xref="taxon:54126"

/clone\_lib="Pristionchus pacificus BAC ends"

## FEATURES

source

1..661

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="var. California"

/db\_xref="taxon:54126"

/clone\_lib="Pristionchus pacificus BAC ends"

## ORIGIN

Query Match 7.9%; Score 121; DB 8; Length 661;  
Best Local Similarity 100.0%; Pred. No. 2.4e-56;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAATGAATTAACGGGGGCCCGCAC 925  
|||||

Db 223 GACCGCTGGGAGTACGCCCGCAAGGTTAAACTCAATGAATTAACGGGGGCCCGCAC 282  
|||||

QY 926 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 985  
|||||

Db 283 AAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACA 342  
|||||

QY 986 T 986  
343 T 343

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2005, 06:04:18 ; Search time 1416 Seconds  
(without alignments)  
650.176 Million cell updates/sec

Title: US-09-979-558A-1\_COPY\_458\_476

Perfect score: 19  
Sequence: 1 cccgggacgatgacatta 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	100.0	19	6	E58428
C 2	19	100.0	193	1	AJ842303
C 3	19	100.0	194	1	AJ842302
4	19	100.0	300	1	AF025555
5	19	100.0	1403	1	AB094456
6	19	100.0	1462	1	AB094458
7	19	100.0	1473	1	PSP551093
8	19	100.0	1473	1	PSP551098
9	19	100.0	1473	1	PSP551101
10	19	100.0	1520	1	AB016059
11	19	100.0	1525	1	AB016056
12	19	100.0	1526	1	AB016057
13	19	100.0	1526	6	E58427
14	19	100.0	1530	1	AB016058
15	19	100.0	1531	1	AB016055
16	19	100.0	1536	1	AB016054
17	19	100.0	1684	1	PSP551107
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19	17.4	91.6	165	1	AF440847

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21	17.4	91.6	170	1	AF440834	AF440834	Unculture
22	17.4	91.6	170	1	AF440837	AF440837	Unculture
23	17.4	91.6	171	1	AF440838	AF440838	Unculture
24	17.4	91.6	172	1	AF128774	AF128774	Unculture
25	17.4	91.6	172	1	AF440831	AF440831	Unculture
26	17.4	91.6	174	1	AF440842	AF440842	Unculture
27	17.4	91.6	175	1	AF440832	AF440832	Unculture
28	17.4	91.6	175	1	AF440846	AF440846	Unculture
29	17.4	91.6	177	1	AF128777	AF128777	Unculture
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31	17.4	91.6	595	1	AY377466	AY377466	Adelie pe
32	17.4	91.6	595	1	AY377467	AY377467	Adelie pe
33	17.4	91.6	595	1	AY377473	AY377473	Adelie pe
34	17.4	91.6	596	1	AY377472	AY377472	Adelie pe
35	17.4	91.6	597	1	AY377471	AY377471	Adelie pe
36	17.4	91.6	599	1	AY377469	AY377469	Adelie pe
37	17.4	91.6	601	1	AY377470	AY377470	Adelie pe
38	17.4	91.6	691	1	AY159801	AY159801	Psychroba
39	17.4	91.6	692	1	AY159792	AY159792	Psychroba
40	17.4	91.6	700	1	PSP244767	PSP244767	Psychroba
41	17.4	91.6	717	1	PSP244768	PSP244768	Psychroba
42	17.4	91.6	880	1	AF513419	AF513419	Psychroba
43	17.4	91.6	914	1	AY494611	AY494611	Unculture
44	17.4	91.6	1354	1	AF505742	AF505742	Bacterium
45	17.4	91.6	1401	1	AF505736	AF505736	Bacterium

## ALIGNMENTS

RESULT 1  
E58428/c  
LOCUS E58428 19 bp DNA linear PAT 31-JAN-2002  
DEFINITION DNA probe for detecting novel psychrophile.  
ACCESSION E58428  
VERSION E58428.1 GI:18622290  
KEYWORDS JP 2000333680-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Maruyama.A., Kitamura.K. and Kurane.R.  
TITLE DNA probe for detecting novel psychrophile  
JOURNAL Patent: JP 2000333680-A 2 05-DEC-2000;  
AGENCY OF IND SCIENCE & TECHNOL  
COMMENT OS Artificial Sequence  
PN JP 2000333680-A/2  
PD 05-DEC-2000  
PF 25-MAY-1999 JP 1999145342  
PR  
PI AKIHIKO MARIYAMA,KEIKO KITAMURA,RYUICHIRO KURANE PC  
C12N15/09,C12N1/20,C12Q1/68//C12N15/09,C12R1/01),(C12N1/20, PC  
PC C12N15/00,(C12N15/00,C12R1/01)  
CC Key Location/Qualifiers  
FT source 1..19  
FT /organism='Artificial Sequence'.  
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source Location/Qualifiers  
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/db\_xref="taxon:32630"

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 19 CCCGGGACGATGACATTA 1

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RESULT 2
AJ842303/c
LOCUS      AJ842303                193 bp    DNA        linear    BCT 12-OCT-2004
DEFINITION unidentified bacterium partial 16S rRNA gene, clone SD33.
ACCESSION  AJ842303
VERSION     AJ842303.1 GI:52839363
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Li, M.
TITLE      A survey of microbial diversity around the Chinese Antarctic
JOURNAL    Research Station and its environmental significance
REFERENCE  2 (bases 1 to 193)
AUTHORS    Li, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-SEP-2004) Li M., Marine Biogenetic Resource
           Laboratory, Third Institute of Oceanography, SOA, 184 Daxue Road,
           Xiamen, Fujian Province, 361005, CHINA
FEATURES   Location/Qualifiers
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              /environmental_sample
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              /gene="16S rRNA"
            rRNA
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Query Match      100.0%; Score 19; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGACGATGACATTA 19
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Db   66  CCCGGGACGATGACATTA 48

RESULT 3
AJ842302/c
LOCUS      AJ842302                194 bp    DNA        linear    BCT 12-OCT-2004
DEFINITION unidentified bacterium partial 16S rRNA gene, clone SD32.
ACCESSION  AJ842302
VERSION     AJ842302.1 GI:52839362
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Li, M.
TITLE      A survey of microbial diversity around the Chinese Antarctic
JOURNAL    Research Station and its environmental significance
REFERENCE  2 (bases 1 to 194)
AUTHORS    Li, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-SEP-2004) Li M., Marine Biogenetic Resource
           Laboratory, Third Institute of Oceanography, SOA, 184 Daxue Road,
           Xiamen, Fujian Province, 361005, CHINA
FEATURES   Location/Qualifiers
            source
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGACGATGACATTA 19
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Db   66  CCCGGGACGATGACATTA 48

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/gene="16S rRNA"
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGACGATGACATTA 19
    |||||
Db   66  CCCGGGACGATGACATTA 48

RESULT 4
AF025555
LOCUS      AF025555                300 bp    DNA        linear    BCT 11-SEP-2000
DEFINITION Psychrobacter glacincola 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF025555
VERSION     AF025555.1 GI:2582456
KEYWORDS   Psychrobacter glacincola
SOURCE     Psychrobacter glacincola
           Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
           Moraxellaceae; Psychrobacter.
REFERENCE  1 (bases 1 to 300)
AUTHORS    Hagstrom, A., Pinhassi, J. and Zweifel, U. L.
TITLE      Biogeographical diversity among marine bacterioplankton
JOURNAL    Aquat. Microb. Ecol. 21, 231-244 (2000)
REFERENCE  2 (bases 1 to 300)
AUTHORS    Pinhassi, J., Zweifel, U. L. and Hagstrom, A.
TITLE      Direct Submission
JOURNAL    Submitted (18-SEP-1997) National Environmental Research Institute,
           Frederiksborgvej 399, Roskilde DK-4000, Denmark
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              /strain="MED12"
              /db_xref="taxon:56810"
              /note="isolated from the NW Mediterranean"
            rRNA
              <1..>300
              /product="16S ribosomal RNA"

ORIGIN
Query Match      100.0%; Score 19; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCCGGGACGATGACATTA 19
    |||||
Db   250  CCCGGGACGATGACATTA 268

RESULT 5
AB094456
LOCUS      AB094456                1403 bp   DNA        linear    BCT 11-DEC-2003
DEFINITION Psychrobacter sp. MJYP.15.12 gene for 16S rRNA, partial sequence.
ACCESSION  AB094456
VERSION     AB094456.1 GI:27807566
KEYWORDS   Psychrobacter sp. MJYP.15.12
SOURCE     Psychrobacter sp. MJYP.15.12
ORGANISM   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
           Moraxellaceae; Psychrobacter.
REFERENCE  1
AUTHORS    Inagaki, F., Suzuki, M., Takai, K., Oida, H., Sakamoto, T., Aoki, K.,
           Nealson, K. H. and Horikoshi, K.
TITLE      Microbial Communities Associated with Geological Horizons in
           Coastal Seafloor Sediments from the Sea of Okhotsk

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us-09-979-558a-1\_copy\_458\_476.rge

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science & Technology Center, Subground Animalcule Retrieval (SUGAR) Project, Frontier Research System for Extremophiles; Natsuchima-cho 2-15, Yokosuka 237-0061, Japan (E-mail:inagaki@jamstec.go.jp, Tel:81-468-67-9687, Fax:81-468-67-9715)  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="MJYP.15.12"  
/isolation\_source="subseafloor sediment"  
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/isolation\_source="subseafloor sediment"  
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/product="16S ribosomal RNA"

ORIGIN  
Query Match 100.0%; Score 19; DB 1; Length 1403;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19  
|||||  
Db 440 CCCGGGACGATGACATTA 458

RESULT 6  
AB094458  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Psychrobacter sp. MJYP.25.32  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE  
AUTHORS  
TITLE  
Inagaki, F., Suzuki, M., Takai, K., Oida, H., Sakamoto, T., Aoki, K., Neilson, K. H. and Horikoshi, K.  
Microbial Communities Associated with Geological Horizons in Coastal Subseafloor Sediments from the Sea of Okhotsk  
Appl. Environ. Microbiol. 69 (12), 7224-7235 (2003)  
14660370  
2 (bases 1 to 1462)  
Direct Submission  
Submitted (23-OCT-2002) Fumio Inagaki, Japan Marine Science & Technology Center, Subground Animalcule Retrieval (SUGAR) Project, Frontier Research System for Extremophiles; Natsuchima-cho 2-15, Yokosuka 237-0061, Japan (E-mail:inagaki@jamstec.go.jp, Tel:81-468-67-9687, Fax:81-468-67-9715)  
Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 19; DB 1; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19  
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Db 438 CCCGGGACGATGACATTA 456

RESULT 7  
PSP551093  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Psychrobacter sp. wp8 partial 16S rRNA gene, isolate wp8.  
AJ551093.1 GI:34525808  
16S ribosomal RNA; 16S rRNA gene.  
Psychrobacter sp. wp8  
Psychrobacter sp. wp8  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE  
AUTHORS  
TITLE  
Wang, F., Wang, P., Chen, M. and Xiao, X.  
Isolation of extremophiles with the detection and retrieval of Shewanella strains in deep-sea sediments from the west Pacific Extremophiles 8 (2), 165-168 (2004)  
15064982  
2 (bases 1 to 1473)  
Xiao, X.  
Direct Submission  
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic Resources, Third Institute of Oceanography, SOA, Daxuelu 178, Xiamen, 361005, CHINA  
Location/Qualifiers  
1..1473  
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/gene="16S rRNA"  
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gene  
rRNA

ORIGIN  
Query Match 100.0%; Score 19; DB 1; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19  
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Db 458 CCCGGGACGATGACATTA 476

RESULT 8  
PSP551098  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Psychrobacter sp. wp18 partial 16S rRNA gene, isolate wp18.  
AJ551098.1 GI:34525813  
16S ribosomal RNA; 16S rRNA gene.  
Psychrobacter sp. wp18  
Psychrobacter sp. wp18  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.

REFERENCE  
AUTHORS  
TITLE  
Wang, F., Wang, P., Chen, M. and Xiao, X.  
Isolation of extremophiles with the detection and retrieval of Shewanella strains in deep-sea sediments from the west Pacific Extremophiles 8 (2), 165-168 (2004)  
15064982  
2 (bases 1 to 1473)  
Xiao, X.  
Direct Submission  
Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic Resources, Third Institute of Oceanography, SOA, Daxuelu 178, Xiamen, 361005, CHINA

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        /gene="16S rRNA"
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gene
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    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
    |||||
Db 458 CCCGGGACGATGACATTA 476

RESULT 9
PSP551101      1473 bp      DNA      linear      BCT 17-MAY-2004
LOCUS
DEFINITION
  Psychrobacter sp. wp21 partial 16S rRNA gene, isolate wp21.
ACCESSION
  AJ551101
VERSION
  AJ551101.1 GI:34525815
KEYWORDS
  16S ribosomal RNA; 16S rRNA gene.
SOURCE
  Psychrobacter sp. wp21
ORGANISM
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
  Moraxellaceae; Psychrobacter.
REFERENCE
  1
  Wang, F., Wang, P., Chen, M. and Xiao, X.
  Isolation of extremophiles with the detection and retrieval of
  Shewanella strains in deep-sea sediments from the west Pacific
  Extremophiles 8 (2), 165-168 (2004)
JOURNAL
  PUBMED
  15064982
AUTHORS
  Xiao, X.
TITLE
  Direct Submission
JOURNAL
  Submitted (22-FEB-2003) Xiao X., Key Lab of Marine Biogenetic
  Resources, Third Institute of Oceanography, SOA, Daxuelu 178,
  Xiamen, 361005, CHINA

FEATURES
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gene
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ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 46;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
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Db 458 CCCGGGACGATGACATTA 476

RESULT 10
AB016059      1520 bp      DNA      linear      BCT 10-MAY-2000
LOCUS
DEFINITION
  Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
  strain:NIH P2K18.
ACCESSION
  AB016059
VERSION
  AB016059.1 GI:6691640
KEYWORDS
  16S ribosomal RNA.
SOURCE
  Psychrobacter pacificensis
ORGANISM
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
  Moraxellaceae; Psychrobacter.
REFERENCE
  1 (sites)
  Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
  Phylogenetic analysis of psychrophilic bacteria isolated from the
  Japan Trench, including a description of the deep-sea species
  Psychrobacter pacificensis sp. nov
  Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
  MEDLINE
  2022194
PUBMED
  10758895
AUTHORS
  Maruyama, A. and Kitamura, K.
TITLE
  Direct Submission
JOURNAL
  Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
  Bioscience and Human-Technology, Department of Applied and
  Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
  Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062,
  Fax:+81-298-54-6412)
FEATURES
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rRNA

ORIGIN
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    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
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Db 454 CCCGGGACGATGACATTA 472

RESULT 11
AB016056      1525 bp      DNA      linear      BCT 10-MAY-2000
LOCUS
DEFINITION
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  strain:NIH P2J13.
ACCESSION
  AB016056
VERSION
  AB016056.1 GI:6691637
KEYWORDS
  16S ribosomal RNA.
SOURCE
  Psychrobacter pacificensis
ORGANISM
  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
  Moraxellaceae; Psychrobacter.
REFERENCE
  1 (sites)
  Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
  Phylogenetic analysis of psychrophilic bacteria isolated from the
  Japan Trench, including a description of the deep-sea species
  Psychrobacter pacificensis sp. nov
  Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
JOURNAL
  MEDLINE
  2022194
PUBMED
  10758895
AUTHORS
  Maruyama, A. and Kitamura, K.
TITLE
  Direct Submission
JOURNAL
  Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
  Bioscience and Human-Technology, Department of Applied and
  Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
  Japan (E-mail:maruyama@nih.go.jp, Tel:+81-298-54-6062,
  Fax:+81-298-54-6412)

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FEATURES
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        Best Local Similarity 100.0%; Pred. No. 46;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
    |||||
Db 455 CCCGGGACGATGACATTA 473

RESULT 12
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LOCUS
DEFINITION
  Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,
  strain:NIBH P2K6(T) (=IFO 16279(T)).
ACCESSION
  AB016057.1 GI:6691638
VERSION
  16S ribosomal RNA.
KEYWORDS
  Psychrobacter pacificensis
SOURCE
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Moraxellaceae; Psychrobacter.
  1 (sites)
  Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
  Phylogenetic analysis of psychrophilic bacteria isolated from the
  Japan Trench, including a description of the deep-sea species
  Psychrobacter pacificensis sp. nov
  Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
  2022194
PUBMED
  10758895
REFERENCE
  2 (bases 1 to 1526)
  Maruyama, A. and Kitamura, K.
  Direct Submission
  Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
  Bioscience and Human-Technology, Department of Applied and
  Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,
  Japan (E-mail:maruyama@nibh.go.jp, Tel: +81-298-54-6062,
  Fax: +81-298-54-6412)
  Location/Qualifiers
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      /mol_type="genomic DNA"
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        Query Match          100.0%; Score 19; DB 1; Length 1526;
        Best Local Similarity 100.0%; Pred. No. 46;
        Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
    |||||
Db 458 CCCGGGACGATGACATTA 476

RESULT 13
E58427
LOCUS
DEFINITION
  DNA probe for detecting novel psychrophile.
ACCESSION
  E58427
VERSION
  E58427.1 GI:18622289
KEYWORDS
  JP 2000333680-A/1.

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SOURCE
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    unidentified
    unclassified.
  1 (bases 1 to 1526)
  Maruyama, A., Kitamura, K. and Kurane, R.
  DNA probe for detecting novel psychrophile
  Patent: JP 2000333680-A 1 05-DEC-2000;
  AGENCY OF IND SCIENCE & TECHNOL
  OS
    Psychrobacter pacificus
  PN
    JP 2000333680-A/1
  PD
    05-DEC-2000
  PF
    25-MAY-1999 JP 1999145342
  PR
  PI
    AKIHIKO MARYAMA, KEIKO KITAMURA, RYUICHIRO KURANE PC
    C12N15/09, C12N1/20, C12Q1/68 // (C12N15/09, C12R1:01), (C12N1/20, PC
    C12R1:01),
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      Best Local Similarity 100.0%; Pred. No. 46;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGACGATGACATTA 19
    |||||
Db 458 CCCGGGACGATGACATTA 476

RESULT 14
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LOCUS
DEFINITION
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  strain:NIBH P2K17.
ACCESSION
  AB016058.1 GI:6691639
VERSION
  16S ribosomal RNA.
KEYWORDS
  Psychrobacter pacificensis
SOURCE
  ORGANISM
    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Moraxellaceae; Psychrobacter.
  1 (sites)
  Maruyama, A., Honda, D., Yamamoto, H., Kitamura, K. and Higashihara, T.
  Phylogenetic analysis of psychrophilic bacteria isolated from the
  Japan Trench, including a description of the deep-sea species
  Psychrobacter pacificensis sp. nov
  Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)
  2022194
PUBMED
  10758895
REFERENCE
  2 (bases 1 to 1530)
  Maruyama, A. and Kitamura, K.
  Direct Submission
  Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of
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## RESULT 15

AB016055 1531 bp DNA linear BCT 10-MAY-2000  
 LOCUS Psychrobacter pacificensis DNA for 16S rRNA, partial sequence,  
 DEFINITION strain:NIBH P2J3.

ACCESSION AB016055

VERSION AB016055.1 GI:6691636

KEYWORDS 16S ribosomal RNA.

SOURCE Psychrobacter pacificensis

ORGANISM Psychrobacter pacificensis

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Moraxellaceae; Psychrobacter.

## REFERENCE

AUTHORS 1 (sites)  
 TITLE Maruyama A., Honda D., Yamamoto H., Kitamura K. and Higashihara T.  
 Phylogenetic analysis of psychrophilic bacteria isolated from the  
 Japan Trench, including a description of the deep-sea species  
 Psychrobacter pacificensis sp. nov  
 JOURNAL Int. J. Syst. Evol. Microbiol. 50 Pt 2, 835-846 (2000)  
 MEDLINE 2022194  
 PUBMED 10758895

## REFERENCE

AUTHORS 2 (bases 1 to 1531)  
 TITLE Maruyama A. and Kitamura K.  
 JOURNAL Direct Submission  
 Submitted (07-JUL-1998) Akihiko Maruyama, National Institute of  
 Bioscience and Human-Technology, Department of Applied and  
 Environmental Microbiology; 1-1 Higashi, Tsukuba, Ibaraki 305-8566,  
 Japan (E-mail:maruyama@nibh.go.jp, Tel:+81-298-54-6062,  
 Fax:+81-298-54-6412)

## FEATURES

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## rRNA

## ORIGIN

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